

XX Hepatitis C virus 1.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /label= ARG
 FT Misc-difference 11 /label= THR
 FT Misc-difference 176 /label= THR
 FT Misc-difference 334 /label= VAL
 FT Misc-difference 603 /label= ILE
 FT Misc-difference 848 /label= (ASN)
 FT Misc-difference 1114 /label= SER
 FT Misc-difference 1117 /label= THR
 FT Misc-difference 1276 /label= LEU
 FT Misc-difference 1328 /label= (VAL)
 FT Misc-difference 1454 /label= TYR
 FT Misc-difference 1471 /label= (SER)
 FT Misc-difference 1877 /label= (GLY)
 FT Misc-difference 1948 /label= (HIS)
 FT Misc-difference 1949 /label= (CYS)
 FT Misc-difference 2021 /label= (VAL)
 FT Misc-difference 2349 /label= (SER)
 FT Misc-difference 2385 /label= (PHE)
 FT Misc-difference 2386 /label= (ALA)
 FT Misc-difference 2502 /label= (PHE)
 FT Misc-difference 2690 /label= (GLY)
 FT Misc-difference 2996 /label= (PRO)
 XX W9205642-A.
 PR
 XX
 PD 20-FEB-1992.
 PF
 XX 12-AUG-1991; 91W0-US05728.
 XX
 PR 10-AUG-1990; 90US-0566209.
 XX
 PA (CHIR-) CHIRON CORP.
 XX
 PI Houghton M, Choo QL, Weiner AJ, Urdea MS, Irvine BD;
 PI Kolberg JA;
 DR
 DR WPI: 1992-080094/10.
 DR N-PSDB: AAQ21744.
 XX
 XX Reagents for isolating, amplifying and detecting HCV
 PI polynucleotide(s) - used to monitor spread of blood-borne non-A,
 PI non-B hepatitis virus infection and screen blood samples for
 PT virus
 XX
 XX Disclosure: Fig 1: 67pp; English.
 OS
 XX Heterogeneities in cloned DNAs of HCV1 are indicated by the amino

CC acid indicated in the features, the parentheses indicated that the
 CC heterogeneity was detected at or near to the 5'- or 3'-end of the
 CC HCV in the clone.
 CC The sequence is derived from a composite HCV cDNA from HCV1, a
 CC prototypic HCV. The DNA sequence is based upon sequence information
 CC derived from a no. of HCV cDNA clones, which were isolated from a no.
 CC of HCV cDNA libraries, including the "c" library present in lambda
 CC gt11 (ATCC No.40394), and from human serum. The HCV cDNA clones
 CC were isolated by methods described in W09014436.
 CC The clones from which the sequence was derived are 5'c10c032,
 CC b114a, 18q, ag30a, CA200a, CA290a, CA216a, p114a, CA167b, CA156e,
 CC CA844a, CA53a, K9-1 (also called K9 1), 26), 13i, 12f, 14i, 11b, 7i,
 CC 7e, 8f, 33c, 48b, 37b, 35, 36, 8i, 32, 34p, 25c, 14c, 8i, 33f, 33q,
 CC 39c, 35f, 19q, 26q, 15c, 65a, 16jh, 6k and p131jh.
 XX
 SQ Sequence 3011 AA:

Query Match 0.5%; Score 59; DB 13; Length 3011;
 Best Local Similarity 34.5%; Prod No. 4 40403;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPAIKFTYKQIKKWNHMGSPMSITQ 1849

1: 111: 1 11 1:1:1

DB 1745 viapavqtnwqkletfwaklmwnfisq 1773

RESULT 200

AAR31621

ID AAR31621 standard; protein; 3011 AA.

XX AAR31621;

AC AAR31621;

XX 24-MAY-1993 (first entry)

ET Hepatitis C virus (HCV) Polyprotein.

XX Hepatitis C virus (HCV) Polyprotein.

XX Hepatitis C virus (HCV) Polyprotein.

KW Hepatitis C virus (HCV) Polyprotein.

KW Hepatitis C virus (HCV) Polyprotein.

OS Hepatitis C virus type 1.

XX Hepatitis C virus type 1.

FH Key Location/Qualifiers

FT Domain 1..191

FT /label= C domain

FT /note= "nucleocapsid protein"

FT Domain 192..383

FT /label= E1

FT /note= "virion envelope protein"

FT Domain 384..800

FT /label= E2/NS1

FT /note= "possible envelope"

FT Domain 800..1050

FT /label= NS2

FT /note= "unknown function"

FT Domain 1050..1650

FT /label= NS3

FT /note= "putative protease domain"

FT Domain 1651..2100

FT /label= NS4

FT /note= "unknown function"

FT Domain 2100..3011

FT /label= NS5

FT /note= "polymerase"

XX W09300365-A.

PN 07-JAN-1993.

XX 24-JUN-1992;

XX 92W0-US05388.

XX 24-JUN-1991;

XX 91US-0732489.

PF

XX AC AAR08123;
 XX DT 23-JAN-1991 (first entry)
 XX DE Hepatitis C virus polypeptide from long ORF.
 XX KW Hepatitis C virus, antiviral agent.
 XX OS Hepatitis C virus.
 XX PN EP388232-A.
 XX PD 19-SEP-1990.
 XX PF 16-MAR-1990; 90EP-0402866.
 XX PK 18 MAY 1989; 89US-0355002.
 XX PR 17-MAR-1989; 89US-0425338.
 XX PR 20-APR-1989; 89US-0441334.
 XX PA (CHIR-) CHIRON CORP.
 XX PI Houghton M, Choo QL, Kuo G;
 XX WP: 1990-284418/38.
 XX N-PSDB; AAQ05955.
 XX PT Hepatitis C virus DNA - used for producing probes,
 XX PI polypeptide(s), antibodies and anti-sense polynucleot-
 XX PS ides for diagnosis and therapy.
 XX PS Disclosure; Fig 16; 63pp, English.
 XX CC HCV cDNA libraries were constructed using pooled serum from a
 XX CC chimpanzee with chronic HCV infection. A lambda gt10 library was
 XX CC screened with probes derived from previously isolated clones. The
 XX CC ORF is derived from the overlapping clones p4a, CA167b, CA156c,
 XX CC CA64a, CA59a, K3-1, 121, 141, 11b, 7f, 9h, 3c, 40b, 37b, 35, 36,
 XX CC 81, 32, 33b, 25c, 14c, 81, 33f, 33g, 39c, 35f, 19g, 26g and 15c.
 XX CC This polypeptide can be used to design probes
 XX CC for the detection of HCV nucleic acids, in screening programmes
 XX CC for antiviral agents and in preparing blood free of HCV. Antisense
 XX CC polynucleotides can be used to inhibit viral replication.
 XX CC See also AAQ05956.
 XX SQ Sequence 2772 AA;
 Query Match 0.5%; Score 59; DB 11; Length 2772;
 Best Local Similarity 34.5%; Pred. No. 3.9e+03;
 Matches 10; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Q7 1821 VLLPAIKETTYEQIEFNKNWENHMPFMSIIQ 1849
 I: ||| :||| | || ||| :|
 Db 1631 viapavqtnwqkletfwakmwnflisqig 1659
 RESULT 192
 AAR18540
 ID AAR18540 standard; Protein: 2772 AA.
 XX AC AAR18540;
 XX DT 15-JAN-2001 (first entry)
 XX DE Protein encoded by a cDNA compiled hepatitis C virus cDNA clones
 XX KW Hepatitis C virus, HCV; antisense polynucleotide; polypeptide;
 XX OS viral infectivity; viral replication
 XX PN Hepatitis C virus.
 XX PD 09-SEP-1992;
 XX PF 92WO-US07683.
 XX PS

PN EP1034785-A2.
 XX PD 13-SEP-2000.
 XX PF 16-MAR-1990; 2000EP-0109602.
 XX PK 17-MAR-1989; 89US-0325338.
 XX PR 20-APR-1989; 89US-0441334.
 XX PR 18-MAY-1989; 89US-0355002.
 XX PR 16-MAR-1990; 90EP-0402866.
 XX PA (CHIR-) CHIRON CORP.
 XX PI Houghton M, Choo Q, Kuo G;
 XX WP: 2000-566891/53.
 XX N-PSDB; AAA75296.
 XX PT Novel composition comprising a hepatitis C virus antisense
 XX PI polynucleotide which is complementary to or corresponds to a sense
 XX PS strand of the virus genome, and selectively hybridises to it -
 XX Example; Fig 16; 75pp; English.
 XX CC The specification describes a pharmaceutical composition which
 XX CC comprises a hepatitis C virus (HCV) antisense polynucleotide. The
 XX CC HCV is characterized by a positive stranded RNA genome which has
 XX CC 40% homology at the polypeptide level to a HCV polypeptide. The
 XX CC antisense polynucleotide binds to cellular polynucleotides which
 XX CC enhance and/or required for viral infectivity, replicative
 XX CC ability or chronicity. The antisense polynucleotides may also be
 XX CC designed to bind with high specificity, to be of increased stability,
 XX CC to be stable and to have low toxicity. The composition also comprises
 XX CC an agent which causes viral RNA to be inactive. The composition
 XX CC is used for preventing HCV replication in a system. The present
 XX CC sequence is encoded by a novel HCV cDNA sequence, which is used in the
 XX CC course of the invention.
 XX SQ Sequence 2772 AA;
 Query Match 0.5%; Score 59; DB 21; Length 2772;
 Best Local Similarity 34.5%; Pred. No. 3.9e+03;
 Matches 10; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Q7 1821 VLLPAIKETTYEQIEFNKNWENHMPFMSIIQ 1849
 I: ||| :||| | || ||| :|
 Db 1631 viapavqtnwqkletfwakmwnflisqig 1659
 RESULT 193
 AAR34009
 ID AAR34009 standard; Protein: 2816 AA.
 XX AC AAR34009;
 XX DT 26-JUL-1993 (first entry)
 XX DE HCV-1 polypeptide.
 XX KW Polymerase chain reaction; PCR, amplify, primer, hepatitis C virus;
 XX KW HCV; asymptomatic; chronically infected; epitope; viral isolate;
 XX KW domain; immunological; cross-reacting; envelope protein; vaccine;
 XX KW 9p53(BVDV); 4p55, hec; cholesta virus; post-hepatitis; NS1, flavivirus.
 XX OS Hepatitis C virus.
 XX PN WQ9406126-A.
 XX PD 01-APR-1993.
 XX PF 11-SEP-1992; 92WO-US07683.
 XX PS

/note- "claimed peptide reactive to HCV antibody"

PT XX JP04288097-A.
 XX 13-OCT-1992.
 XX 07-NOV-1991; 91JP-0401705.
 XX 07-NOV-1991; 91JP 0301705.
 XX (CHAU) CHYMUS OPTICAL Co Ltd.
 XX WPI, 1992 067721/47.
 XX New peptide(s) are reactive to an antibody against type C
 PT hepatitis virus, used to detect virus in patients
 XX Disclosure; Fig 1; 11pp; Japanese.
 XX The peptides (claimed) can be used to detect hepatitis C virus (HCV)
 CC antibody positive patients, post-transfusion hepatitis can be prevented
 CC by screening a sample from a HCV antibody positive patient with the
 CC peptide.
 XX Sequence 2436 AA;
 SQ
 Query Match 0.5%; Score 55; DB 13; Length 2436;
 Best Local Similarity 34.5%; Pred. No. 3,36+03;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1821 VLLDAIKKTYGQIEKRWKHNHMFPMSTILQ 1849
 DB 1295 VIAPGQTWQKLETFWKKHWMTTISGIQ 1923
 RESULT 187
 AAP90288
 ID AAP90288 standard; protein; 2452 AA.
 AC AAP90288;
 DT 01-NOV 1989 (first entry)
 DE Peptide encoded by composite hepatitis C cDNA.
 EW Hepatitis C virus; clone 15c; clone K9-1; probe; vaccine.
 XX Pan troglodytes.
 XX G82212511-A.
 XX 26-JUL-1989.
 XX 18-NOV-1988; 88GB-0027624.
 XX 18-NOV-1987; 87US-0122714.
 XX (CHUR) CHUROR CONTRACTOR.
 XX Houghton M, Choo QL, Kuo G;
 XX WPI; 1989-215054/30.
 XX N-PSDB; AAN90336.
 PT Hepatitis C virus gene - used for produ. of polynucleotide probes,
 PT polypeptide(s) and antibodies for diagnosis, prevention and
 PT treatment of infection.
 XX Disclosure; fig 47-1 to 47-8; 245pp; English.
 XX The sequence is the peptide encoded by the composite hepatitis C
 CC virus (HCV) cDNA of AAN90336. The polypeptides are used to

CC diagnose HCV-induced NANBH, to raise antibodies for
 CC immunosay or treatment, or to produce vaccines.

SQ Sequence 2462 AA;

Query Match 0.5%; Score 59; DB 10; Length 2462;
 Best Local Similarity 34.5%; Pred. No. 3,36+03;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLDAIKKTYGQIEKRWKHNHMFPMSTILQ 1849

DB 1321 VIAPGQTWQKLETFWKKHWMTTISGIQ 1849

RESULT 188

AAR81730

ID AAR81730 standard; protein; 2549 AA.

AC AAR81730;

DT 29 MAY-1996 (first entry)

DE Sirolimus effector protein.

KW Glutathione-S-transferase; GST; FK506 binding protein; FKBP; PKC;
 KW rapamycin; FKBP-rapamycin binding protein; Mol14 cell; amplif;
 EW fusion protein; GST-FKBP12; immunomodulatory agent; primer;
 KW antitumor agent; detection, antisense DNA; immune system.

OS Homo sapiens.

DN EP676471-A2.

DB 11-OCT-1995.

XX 07-MAR-1995; 95EP-0301475.

XX 13-FEB-1995; 95US-0384524

XX 08-MAR-1994; 94US-0207975.

XX 26-SEP-1994; 94US-0312023.

XX (AMHP) AMERICAN HOME PROD CORP.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Caggiano TJ, Chen Y, Failli AA, Molnar-Kimber KL;

XX Nakanishi K;

XX WPI; 1995-346091/45.

XX N-PSDB; AAI00770.

PT New effector proteins of rapamycin - which bind to a
 PT glutathione S-transferase FK506 binding protein-rapamycin complex

XX Example 2; Page 16-29; 44pp; English.

XX This sequence represents the sirolimus effector protein (SEP). The
 CC cDNA encoding this sequence was isolated from Mol14 human T-cell
 CC leukemia cells (ATCC CCL 1582) and used in the production of a fusion
 CC protein between glutathione S transferase (GST) and SEP. The sep gene
 CC was amplified in five fragments using the primers given in AAT00756-69.
 CC The amplified SEP gene was inserted into a vector already containing
 CC the GST gene and the fusion protein expressed (see also AAR81731). The
 CC fusion protein was used in the isolation of a protein of mammalian
 CC origin which binds a glutathione-S-transferase (GST)-FK506 binding
 CC protein (FKBP) rapamycin complex. The FKBP-rapamycin binding protein
 CC and corresponding DNA was isolated from Mol14 cells using a complex of
 CC the fusion protein GST FKBP12 and rapamycin. The isolated proteins have
 CC molecular weights of 125, 148, 208 and 210 kD. They can be used for
 CC identifying an immunomodulatory, or an antitumor agent. They can also
 CC be used in the detection of rapamycin, rapamycin analogues or
 CC metabolites when complexed with FKBP. Antisense DNA can be used to
 CC modulate the immune system of a mammal


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XX OS Poliovirus.
XX PR W09203538 A.
XX PA
XX PT 05-MAR-1992.
XX DR 20-AUG-1991; 91W0-0305850.
XX PR 20-AUG-1990; 90US-0570000.
XX PR 20-AUG-1990; 90US-0569916.
XX PA (NYNY ) 9402BMB1A HIV NEW Y.
XX PI Kananollo V, Tatem JM, Weeks-Lowy CL.
XX PR WPI: 1992 096882/12.
XX DR N-PSDB: AAO22965.
XX PT New vaccine against infectious polio virus comprises RNA virus
XX PI for producing RNA virus cDNA and viable RNA virus
XX PS Disclosure: Fig 6; 110pp; English.
XX CC The protein sequence was deduced from the cDNA sequence of P3
XX CC poliovirus obtained as in AAO22965. The cDNA sequence is that of a
XX CC true RNA virus, i.e. the cDNA directs the production of a viable
XX CC RNA virus which is phenotypically similar to the source virus.
XX CC The full length cDNA in pIBD3 was infectious. In vitro
XX CC transcription of pIBD3 cDNA using T7 RNA polymerase produced
XX CC RNAs which possessed several erroneous amino acids. The RNA
XX CC viruses are used in vaccines against polio. The screening method
XX CC can be used during amplification of the source virus for vaccine
XX CC production to ensure maintenance of C at position 2493 in the viral
XX CC genome, i.e. increasing the attenuation. The new prod. overcomes
XX CC the problem of errors introduced during replication of ss RNA,
XX CC which is much higher than for ds DNA.
XX SQ Sequence 2206 AA;

Query Match 0.5%; Score 59; DB 13; Length 2206;
Best Local Similarity 21.6%; Pred. No. 2,80+03;
Matches 17; Conservative 17; Mismatches 47; Indels 0; Gaps 0;

QY 481 TELMLSLMHLAPVLLANHLKEIMKTSKEVHLSFKEAVLAEGLHGHVVLGALSA 540
DB 621 kaveqlapafedqgthvqprarsesiesffarqacvatiezmqpttraqk1 680
QY 541 FEIKREHFSSEVTISMNLGF 561
DB 681 famwrltykdtuqlrklcft 701

RESULT 182
AAP90164
ID AAP90164 standard; protein; 2261 AA.
XX AC AAP90164;
XX CC 01-NEW 1989 (first entry)
XX DE Peptide encoded by composite hepatitis C virus cDNA.
XX DR Hepatitis C virus, clone 12f, alone 15c, prote. vaccine.
XX OS Pan troglodytes.
XX PR GB2212511-A.
XX DR 26-JUL-1989.
XX PR 18-NOV-1989; 88GB-0027024.

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XX PR 18-NOV-1987; 87US-0122714.
XX PA (CHIR ) CHIRON CORPORATION.
XX PT Houghton M, Choo QL, Kuo G;
XX DR WPI: 1990-215054/30.
XX DR N-PSDB: AAN90331.
XX CC Hepatitis C virus gene - used for prodn. of polynucleotide probes,
XX CC polypeptide(s) and antibodies for diagnosis, prevention and
XX CC treatment of infection.
XX PS Disclosure: Fig 32; 235pp; English.
XX CC The sequence is the peptide encoded by the composite hepatitis C
XX CC virus (HCV) cDNA of AAN90331. The polypeptides are used to diagnose
XX CC HCV-induced NANBH, to raise antibodies for immunoassay or treatment,
XX CC or to produce vaccines.
XX SQ Sequence 2261 AA;

Query Match 0.5%; Score 59; DB 10; Length 2261;
Best Local Similarity 34.5%; Pred. No. 2,60+03;
Matches 30; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPAIKRTYKQIKENWENHMGPPMSILQ 1849
DB 1113 : : : : : : : : : : : : : : : :
DB 1110 viapaypwkletfwakhmwntisq1q 1148

RESULT 183
AAP92047
ID AAP92047 standard; protein; 2401 AA.
XX AC AAP92047;
XX CC 02-MAR-1990 (first entry)
XX DE Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones
XX CC 12f through 15c.
XX KW Hepatitis C virus (HCV); non-A, non-B hepatitis (NANBH)
XX OS Hepatitis C virus.
XX PR EP318216-A.
XX PD 31-MAY-1989.
XX PR 18-NOV-1988; 88EP-0310922.
XX PR 14-NOV-1988; 88US 0271450; US-122714.
XX PA (CHIR ) CHIRON CORP.
XX PI Houghton M, Choo q-L, Kuo G;
XX DR WPI: 1990 150274/23.
XX DR N-PSDB: AAN92103.
XX CC Purified hepatitis C virus
XX CC - and associated nucleic acids and polypeptide(s)
XX PS Claim 13; Figure 32-1 - 32-7; 139 pp; English.
XX CC It is the sequence encoded in the open reading frame of hepatitis C virus
XX CC (HCV) cDNA inserts in clones 12f through 15c. It is antigenic and could
XX CC be used in immunoassay reagents and vaccines and to generate antibodies
XX CC useful in diagnosis and passive immunotherapy for HCV infection/non-A,
XX CC non-B hepatitis.

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[illegible]

Dd		232 presip 237
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RESULT 180		
AAW98454		
ID	AAW98454 standard; Protein: 1767 AA.	
XX AC AAW98454;		
XX 21-MAR-1999 (first entry)		
DE DE H. pylori GIPO 749 protein,		
XX GIPO protein; Helicobacter infection; gastroduodenal disease; gastritis; KW peptic ulcer disease.		
XX Helicobacter pylori.		
GS W0984476-AI.		
PX PN U8-JUL-1998.		
XX O1-APR-1998:	98WC-US06471.	
FF XX 29-JUL-1997:	97US-0502615.	
PR 01-APR-1997:	97US-0834457.	
DR 24-JUN-1997:	97US-0881227.	
XX (HUMAN) HUMAN GIPD 3C1 INCL CA (INMP) MEPTEX-PAVAX PASTEUR MEDICAL SERUMS. XX AI-Garasi A. Kleintous B. Miller C. Sedet BL Conto L DE WTG Y6P 5427A46. N-PSDH: AAK14073. <hr/>		
New isolated helicobacter polynucleotides - used to develop products for the diagnosis prevention and treatment of helicobacter infections and gastrointestinal diseases Claim 8; Page 510-518; 2954pp; English. <hr/>		
This sequence represents a Helicobacter pylori giipr protein of the infection. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including gastric chronic atrophic gastritis, and peptic ulcer diseases, oral gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis. <hr/>		
SQ Sequence	1767 AA;	
<hr/>		
Query Match	95%	Score 59; DR 19; Length 1767;
Best Local Similarity	36.7%; Prot NO 2, Inc-03;	
Matches 11; Conservative 11; Mismatches 6; Indels 0; Gaps		
CZ VLEKSGEKEVEEETFEHEGLEEFIEFEEY		
EEL ELEEELLELELELLELELELE		
Dd 567 refinedrefinedepidermofemurq	596	
<hr/>		
RESULT 181		
AAR22210		
ID AAR22210 standard; Protein: 2236 AA.		
XX AC AAR22210;		
XX 14-JUL-1992 (first entry)		
DE True type 3 poliovirus protein from HEPL		
XX RNA virus; error reduction.		


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XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 480 viapavpwnkietwkwkwnwntisq 508
XX
XX the present invention describes recombinant Hepatitis C virus (HCV)
XX antiserum (1). (1) is useful as a reagent for the detection of antibodies
XX and infection in body fluids from individuals exposed to HCV. The HCV
XX assay uses recombinant HCV antigen, recombinant HCV antibodies and methods to accurately
XX detect the presence of HCV antibodies in samples obtained from
XX individuals suspected of having HCV infection. AAF42215 to AAF42215,
XX AAF42215 to AAF42215 and AAF42215 to AAF42215 represent sequences used
XX in the preparation of the present invention.
XX
XX Sequence: 859 AA
XX
XX Query Match: 85.5% (Score 69); DB 10; Length 859;
XX Best Local Similarity: 34.5% (Prod. No. 7.20002);
XX Matches: 10; Conservative: 0; Mismatches: 10; Indels: 0; Gaps: 0;
XX
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 480 viapavpwnkietwkwkwnwntisq 508
XX
XX RESULT 169
XX AAF42215
XX ID AAF42215 standard; protein: 859 AA.
XX
XX AAF42215
XX
XX 09 AUG 1994 (first entry)
XX
XX Alpha-LNA polymerase.
XX
XX Clone: DNA polymerase; hybridise; amplification; genetic engineering;
XX PCR; polymerase chain reaction; restriction map; plasmid.
XX
XX Sulfotobos sulfatarius.
XX

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XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 480 viapavpwnkietwkwkwnwntisq 508
XX
XX RESULT 168
XX AAF42215
XX ID AAF42215 standard; protein: 859 AA.
XX
XX AAF42215
XX
XX 02 MAR 1999 (first entry)
XX
XX Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones
XX 40b, 47b, 45, 46, 81, 42, 43b and 25c.
XX
XX Hepatitis C virus (HCV); non-A, non-B hepatitis (NANBH)
XX
XX Hepatitis C virus.
XX
XX EP318216-A.
XX
XX 31 MAY 1989.
XX
XX 18-NV-1989; 88EP 0410922.
XX
XX 14-NV-1989; 88US-0271450; (S-122714.
XX
XX (CHIR) CHIR-N CORP.
XX
XX Haughton M. Clasc Appl. Kuo G.
XX
XX WPI: 1989-159274/22.
XX
XX N-PSUB; AAF42085.
XX
XX Purified hepatitis C virus
XX - and associated nucleic acids and polypeptides)
XX
XX Claim 13: Figure 14-A, 14-B, 14-C; 13pp; English.
XX
XX It is the sequence encoded in the open reading frame of hepatitis C virus
XX (HCV) cDNA inserts in clones 40b, 47b, 45, 46, 81, 42, 43b and 25c. It is
XX an epitope which could be used as immunosay reagents and vaccines and
XX to generate antibodies useful in diagnosis and passive immunotherapy for
XX HCV infection/non-A, non-B hepatitis.
XX
XX Sequence: 859 AA:
XX
XX Query Match: 85.5% (Score 69); DB 10; Length 859;
XX Best Local Similarity: 34.5% (Prod. No. 7.20002);
XX Matches: 10; Conservative: 0; Mismatches: 10; Indels: 0; Gaps: 0;
XX
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 1221 VLPAAIRKIKYKLEIKENWKNHMHHSILQ 1649
XX 480 viapavpwnkietwkwkwnwntisq 508
XX
XX RESULT 169
XX AAF42215
XX ID AAF42215 standard; protein: 859 AA.
XX
XX AAF42215
XX
XX 09 AUG 1994 (first entry)
XX
XX Alpha-LNA polymerase.
XX
XX Clone: DNA polymerase; hybridise; amplification; genetic engineering;
XX PCR; polymerase chain reaction; restriction map; plasmid.
XX
XX Sulfotobos sulfatarius.
XX

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Qy 1821 VILLPATKTKTYQ²LEKNWKNHMC²PM²SLIQ 1849
 1 : 11: : : 1 + 11 : : 1 :
 Db 585 viapavqtnwqkletfwakhmwofisq 613

IP AAR21565 standard; Protein; 781 AA.

AA822208	
ID	AA822208 standard; Protein; 781 AA.
XX	
AC	AA822208;
XX	
ET	23-JUL-1992 (first entry)
XX	
DE	Sequence of fusion protein HCV CKS-34-BCD recombinant antigen encoded by pHCV-31.
DE	

XX
KW
CKS fusion protein; antigen.

XX Hepatitis.

XX
PN
EP475182-A.

XX
PD 18-MAR-1992.

XX
PF 26-AUG-1991; 91EP-0114296.

XX
PR 24-AUG-1990; 90US-0573103.

XX
PA (ABCO) ABBOTT LABORATORIES.

XX Holling T.J., Mandecki W:
PI

WP1: 1992-089871/12.

DR N-PSDB; AAQ22963.
XX

Group	hepatitis C virus (HCV) fusion	control	hepatitis C virus (HCV) fusion
PT	control	hepatitis C virus (HCV) fusion	control

Example: Fig 8-40pp. Eccl is

Example, 1990, topp, merged
XX
Z

CC CKS method has been disclosed

together and cloned as a 466
nucleotides representing
pRS fusion vector: 610200

protein HCV CKS Core, consists

construct the plasmid pHCV-3

CC Fragment from pUC19

which consists of 239 AAS of

contributed by linker DNA sequences, 240 AAS at Plo H

CC (AMS 1576-1931), and 10 additional sequences.

XX	sequence	781 AA;
SQ		

Query Match	0.58;
Best Local Similarity	34.58,

Matches 10; Conservative

Q7 1821 VLLPALKKTYKQIERKNWKNHMGE
| : | | : : : | | |

Db 585 viapavqtnwqkletfwakhmwi

RESULT 162

AA33632
ID AA33632 standard; Protein;

1000 JOURNAL OF POST KEYNESIAN ECONOMICS

DT 01-JUN-1993 (first entry)
 XX HCV C100D2 recombinant antigen encoded by pHCV 58.
 DE
 XX
 KW Hepatitis C virus, NS3, C100 antigen, CKS fusion protein;
 KW CMF-K100 synthetase; immunodot assay; Non-A, non-B Hepatitis.
 XX
 OS Hepatitis C virus.
 XX
 PN W09304087-A.
 XX
 PD 04-MAR-1993.
 XX
 XX 21-AUG-1992; 92WO-0507187.
 XX 21-AUG-1991; 91US-0748566.
 XX (ABBO) ABBOTT LAB.
 XX Casey JM, Desai SM, Devare SG. Paperwork 89;
 PT WPI: 1993-093941/11.
 DR N-PSDB; AAQ38258.
 XX
 AS Hepatitis C assay using recombinant C-100 region antigens - for
 PT detecting antibodies and antigen in body fluids from individuals
 PT exposed to hepatitis C virus
 XX
 PG Example 8; Page 93-95; 175pp; English.
 XX
 CC The clone pHCV-58 was constructed to overcome poor expression
 CC levels of the HCV CKS c100 recombinant antigen. HCV CKS-c100
 CC antigen consists of 239 amino acids of CKS, eight amino acids
 CC contributed by linker DNA sequences, 363 amino acids from HCV NS4
 CC region (amino acids 1569-1931) and 10 additional amino acids
 CC contributed by linker DNA sequences. A 63bp NlaIV-HaeIII fragment
 CC was deleted from pHCV-24 (a plasmid which expresses the HCV CKS-
 CC c100 antigen under control of the lac promoter). The pHCV-58
 CC fusion protein (containing a 21 amino acid deletion, i.e. of HCV
 CC amino acids 1609-1620) was expressed at a significantly higher
 CC level than the pHCV-24 fusion protein.
 XX
 SQ Sequence 599 AA;
 Query Match 0.5%; Score 59; DB 14; Length 599;
 Best Local Similarity 34.5%; Pred. No. 4.3e+02;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1921 VLLPAIKTYKQIEKNWKNHMGPEMSIIQ 1849
 DB 403 viapavqlnwqklettakwnwntfsiq 431
 RESULT 156
 AAR33601
 ID AAR33601 standard; Protein: 599 AA.
 XX
 AC AAR33601;
 XX
 DT 05-JUL-1993 (first entry)
 XX
 DE HCV C100D2 recombinant antigen encoded by pHCV-58.
 XX
 KW Hepatitis C virus; non-A, non-B hepatitis virus; NANBH;
 KW non-structural protein, CMF K100 synthetase; CKS fusion protein;
 KW CMF-K100 synthetase; immunodot assay; Non-A, non-B Hepatitis;
 XX
 OS Hepatitis C virus.
 XX
 PN W09304088-A.
 XX

PD 04-MAR-1993.
 XX
 XX 21-AUG-1992; 92WO-0507188.
 XX 21-AUG-1991; 91US-0748561
 XX (ABBO) ABBOTT LAB.
 XX Bailey SM, Desai SM, Devare SG;
 PT WPI: 1993-093941/11.
 DR N-PSDB; AAQ38258.
 XX
 PT Hepatitis C assay using recombinant NS1 region antigens - for
 PT detecting antibodies and antigen in body fluids from individuals
 PT exposed to hepatitis C virus
 XX
 PG Example 8; Page 93-95; 175pp; English.
 XX
 CC The clone pHCV-58 was constructed to overcome poor expression
 CC levels of the HCV CKS-c100 recombinant antigen. HCV CKS-c100
 CC antigen consists of 239 amino acids of CKS, eight amino acids
 CC contributed by linker DNA sequences, 363 amino acids from HCV NS4
 CC region (amino acids 1569-1931) and 10 additional amino acids
 CC contributed by linker DNA sequences. A 63bp NlaIV-HaeIII fragment
 CC was deleted from pHCV-24 (a plasmid which expresses the HCV CKS-
 CC c100 antigen under control of the lac promoter). The pHCV-58
 CC fusion protein (containing a 21 amino acid deletion, i.e. of HCV
 CC amino acids 1609-1620) was expressed at a significantly higher
 CC level than the pHCV-24 fusion protein.
 XX
 SQ Sequence 599 AA;
 Query Match 0.5%; Score 59; DB 14; Length 599;
 Best Local Similarity 34.5%; Pred. No. 4.3e+02;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 1821 VLLPAIKTYKQIEKNWKNHMGPEMSIIQ 1849
 DB 403 viapavqlnwqklettakwnwntfsiq 431
 RESULT 157
 AAB51379
 ID AAB51379 standard; Protein: 599 AA.
 XX
 AC AAB51379;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE HCV recombinant antigen pHCV-58 protein sequence SEQ ID NO:18.
 XX Hepatitis C virus; HCV; antigen; detection; antibody.
 XX
 OS Hepatitis C virus.
 XX
 PN US6172189-B1.
 XX
 PD 09-JAN-2001.
 XX
 XX 02-JUN-1997; 97US-0867611.
 XX
 PR 19-NOV-1982; 92US-0909843.
 PR 10-JAN-1994; 94US-0179896.
 PR 01-MAY-1996; 96US-0646757.
 PR 24-APR-1990; 90US-0572822.
 PR 07-NOV-1990; 90US-0614069.
 PR 21-AUG-1991; 91US-0748561.
 PR 21-AUG-1991; 91US-0748561.
 PR 29-OCT-1991; 91US-0748565.
 XX
 PA (ABBO) ABBOTT LAB.

the clone pHCV 57 was constructed to overcome poor expression levels of the HCV NS5b recombinant antigen. HCV NS5b antigen consists of 239 amino acids of NS5, eight amino acids contributed by linker DNA sequences, 263 amino acids from HCV region (amino acids 1569-1941) and 10 additional amino acids contributed by linker DNA sequences. A 60bp *NotI* fragment was deleted from pHCV-24 to a plasmid which expresses to HCV NS5.

Query Match: 0.58 Score: 59 OR 22; length 597;

PT Human monoclonal anti-HCV antibody, tissue growth, antigen/antibody
XX anti-HCV antibody, tissue growth, antigen/antibody

XX Claim 1: Page 53-55; 206pp; English.

XX A specific antigenic portion of the HCV genome is expressed as a
XX fusion protein with a polypeptide tag. The tag is used to detect the

XX in body fluids from individuals exposed to HCV. In
XX confirmatory, competition or neutralisation assays.

XX Sequence 592 AA:

Query Match 0.5% Score 59; 98 14; Length 592

Best local similarity 44.5% Prod. No. 420024

Matches 10; Conservative 9; Mismatches 16; Gaps 0

QY 1821 VLDLALKEIKYVTEKNNFNDHMDPNSIIQ 1849

IR 401 VLDLALKEIKYVTEKNNFNDHMDPNSIIQ 429

RESULT 145

AA69023

ID AA69023 standard: Peptide: 592 AA.

AC AA69023

XX 17-APR-2001 (first entry)

XX HCV recombinant antigen pBV 62 amino acid sequence SEQ ID NO:47.

XX Hepatitis C virus: HCV; antigen: detection; antibody.

XX Hepatitis C virus.

XX US6172189-B1.

XX 09-JAN-2001.

XX 02-JUN-1997; 97US-0867611.

XX 19-NOV-1994; 92US-0989843.

XX 10-JAN-1994; 94US-0179896.

XX 24-MAY-1996; 96US-0646757.

XX 24-AUG-1990; 90US-0572822.

XX 07-NOV-1990; 90US-0614069.

XX 21-AUG-1991; 91US-0748561.

XX 21-AUG-1991; 91US-0748566.

XX 29-OCT-1991; 91US-0748565.

XX (ABB0) ABBOTT LAB.

XX In-care SM, Casey SM, Barry SM, Lawson GL, Galanter KA;

XX Lesniowski KK, Stewart JL, Supprecht KK;

XX WPI 2001 122352713.

XX New recombinant antigens representing distinct antigenic regions of

XX Hepatitis C virus (HCV) genome, useful for detection of antibodies and

XX antigens in body fluids of individuals exposed to HCV.

XX Example 16; Column 174-178; 147pp; English.

XX The present invention describes recombinant Hepatitis C virus (HCV)

XX A specific antigenic portion of the HCV genome is expressed as a

XX fusion protein with a polypeptide tag. The tag is used to detect the

XX in body fluids from individuals exposed to HCV. In

XX confirmatory, competition or neutralisation assays.

XX Sequence 592 AA:

Query Match 0.5% Score 59; 98 14; Length 592

Best local similarity 44.5% Prod. No. 420024

Matches 10; Conservative 9; Mismatches 16; Gaps 0

QY 1821 VLDLALKEIKYVTEKNNFNDHMDPNSIIQ 1849

IR 401 VLDLALKEIKYVTEKNNFNDHMDPNSIIQ 429

RESULT 145

AA69023

ID AA69023 standard: Peptide: 592 AA.

AC AA69023

XX 17-APR-2001 (first entry)

XX HCV recombinant antigen pBV 62 amino acid sequence SEQ ID NO:47.

XX Hepatitis C virus: HCV; antigen: detection; antibody.

XX Hepatitis C virus.

XX US6172189-B1.

XX 09-JAN-2001.

XX 02-JUN-1997; 97US-0867611.

XX 19-NOV-1994; 92US-0989843.

XX 10-JAN-1994; 94US-0179896.

XX 24-MAY-1996; 96US-0646757.

XX 24-AUG-1990; 90US-0572822.

XX 07-NOV-1990; 90US-0614069.

XX 21-AUG-1991; 91US-0748561.

XX 21-AUG-1991; 91US-0748566.

XX 29-OCT-1991; 91US-0748565.

XX (ABB0) ABBOTT LAB.

XX In-care SM, Casey SM, Barry SM, Lawson GL, Galanter KA;

XX Lesniowski KK, Stewart JL, Supprecht KK;

XX WPI 2001 122352713.

XX New recombinant antigens representing distinct antigenic regions of

XX Hepatitis C virus (HCV) genome, useful for detection of antibodies and

XX antigens in body fluids of individuals exposed to HCV.

XX Example 16; Column 174-178; 147pp; English.

XX The present invention describes recombinant Hepatitis C virus (HCV)

XX 24-JUN-1998; 98JP-0193788.
 XX (SEK) ; SEIKAGAKO Kogyo Co Ltd.
 XX WPI: 2000-140125/13.
 XX A hyaluronate synthase modified protein - useful as a research reagent
 PT for biochemical research and medical development
 XX Claim 12; Page : 30pp; Japanese.
 XX The present invention describes a recombinant protein which consists of
 CC three continuous regions (N-terminal region, internal region and
 CC C-terminal region) where one or two regions among the above three
 CC regions is selected from the three hyaluronate synthase (HAS) modified
 CC proteins HAS1, HAS2 and HAS3 (e.g., a protein made from HAS1 amino acids
 CC 1 to 71, HAS2 amino acids 52 to 379 and HAS3 amino acids 410 to 583).
 CC The protein is useful as a research reagent for biochemical research
 CC and medical development. The invention provides a HAS modified protein
 CC of increased or lowered activity. AAY78127 to AAY78142 represent
 CC specifically claimed examples of recombinant proteins from the present
 CC invention.
 CC N.B. The present sequence is not given in the present specification,
 CC but is derived from sequences given as specified in the claim.
 XX Sequence 553 AA;

Query Match 0.5%; Score 59; DB 21; Length 553;
 Best Local Similarity 28.6%; Pred No. 46002;
 Matches 14; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 973 VTCUATFEFFLOPKFKSKHCKISPTFNILSVSYSPSYIAKIMKV 1021
 DB 58 LKqLafchukmkzkdjfkknkzckdcaayepdpyirkzlpz 106

RESULT 142

AA78127
 ID AAY78127 standard; Protein: 573 AA.
 AC AAY78127;
 DT 27-APR 2000 (first entry)
 XX Recombinant chimeric hyaluronate synthase modified protein #1.
 DE Mouse; murine; hyaluronate synthase; modification: HAS1; HAS2; HAS3;
 KW research reagent; biochemical research; medical development; chimeric.
 XX Chimeric. Mus sp.
 CS Synthetic.
 XX JP2930804886-A.
 XX 11-JAN-2000.
 XX 24-JUN 1998; 98JP 0193788.
 XX 24-JUN-1998; 98JP-0193788.
 XX (SEK) SEIKAGAKO KOGYO CO LTD.
 XX WPI: 2000-140125/13.

XX A hyaluronate synthase modified protein - useful as a research reagent
 PT for biochemical research and medical development
 XX Claim 2; Page : 30pp; Japanese.
 XX The present invention describes a recombinant protein which consists of
 CC three continuous regions (N-terminal region, internal region and

CC C-terminal region) where one or two regions among the above three
 CC regions is selected from the three hyaluronate synthase (HAS) modified
 CC proteins HAS1, HAS2 and HAS3 (e.g., a protein made from HAS1 amino acids
 CC 1 to 71, HAS2 amino acids 52 to 379 and HAS3 amino acids 410 to 583).
 CC The protein is useful as a research reagent for biochemical research
 CC and medical development. The invention provides a HAS modified protein
 CC of increased or lowered activity. AAY78127 to AAY78142 represent
 CC specifically claimed examples of recombinant proteins from the present
 CC invention.
 CC N.B. The present sequence is not given in the present specification,
 CC but is derived from sequences given as specified in the claim.
 XX Sequence 573 AA;

Query Match 0.5%; Score 59; DB 21; Length 573;
 Best Local Similarity 28.6%; Pred No. 46002;
 Matches 14; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 973 VTCUATFEFFLOPKFKSKHCKISPTFNILSVSYSPSYIAKIMKV 1021
 DB 78 LKqLafchukmkzkdjfkknkzckdcaayepdpyirkzlpz 126

RESULT 143

AA78127
 ID AAY94928 standard; Protein: 590 AA.

AC AAY94928;

DT 16-JUN-2000 (first entry)

DE Human secreted protein clone p9195.1 protein sequence SEQ ID NO:62.

XX Human; secreted protein; immunostimulant; immunosuppressant; virucide;
 KW antitubercular; antifungal; cytostatic; anti-inflammatory; dermatological;
 KW antidiabetic; antiasthmatic; antiarthritic; antineumatic; protozoicide;
 KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
 KW infection, HIV, hepatitis, malaria; autoimmune disorder; systemic lupus;
 KW connective tissue disease; multiple sclerosis; erythematosis;
 KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KW insulin dependent diabetes mellitus; graft-versus-host-disease;
 KW autoimmune inflammatory eye disease; allergy.

XX Homo sapiens.

XX WO200000552-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 98WO-018298.

XX 14-AUG-1998; 98US-0096622.

XX 17-AUG-1998; 98US-0096815.

XX 04-SEP-1998; 98US 6094229.

XX 23-OCT-1998; 98US-0105368.

XX 08 JAN-1999; 98US-0115234.

XX 12-FEB-1999; 98US-0119431.

XX 18-FEB-1999; 98US-0120575.

XX 30-APR-1999; 98US-0132020.

XX 11-AUG-1999; 98US-0096622.

XX (GEMV) GENETICS INST INC.

XX Jacobs K, McCoy JM, LaVallic ER, Collins-Pardo JA, Evans G;

PI Merberg D, Treacy M, Aostino MJ, Steininger RJ, Spaulding V;

PI Wong GG, Clark HF, Fechtel K;

XX WPI: 2000-205979/18.

XX few polynucleotides encoding secreted proteins, which may have e.g.,
 PT nutritional, chemokine, immune stimulating or suppressing,

XX
XX

AA	
SQ	Sequence: 460 AA;

RESULT 129
AAY35345


```

XX  New A non B hepatitis, pre-S1 vaccine, diagnosis;
KW passive immunotherapy; antigen.
XX  Hepatitis C virus.
XX  Key: Location/Qualifiers
FT Region 1..27
FT /Label: 336
FT Region 28..42
FT /Label: adaptor
FT Region 43..377
FT /Label: NAB
FT Region 378..382
FT /Label: extra
XX  EP112216.A.
XX  31 MAY 1989.
XX  18-NOV-1988; 88EP-0310922.
XX  14-NOV 1988; 88US 9271450.
XX  (CHIR-) CHIRON CORP
XX  Houghton M, Choo QL, Kuo G;
XX  WP1: 1989-159274/22.
XX  N-PSDB; AAN92104.
XX  Purified hepatitis C virus -
XX  and assorted nucleic acids and polypeptide(s)
XX  Example, Fig 16.1, 16.2, 17pp, English.
XX  Purified hepatitis C virus (HCV) and purified or recombinant HCV nucleic
XX  acids (NAs), encoding HCV polypeptides or epitopes, and polypeptides
XX  are claimed. HCV is a causative agent of non A, non B hepatitis (NANBH).
XX  The NAs may be used to design probes for detection of HCV NAs in samples.
XX  The polypeptides may be used as immun assay reagents and vaccines, and
XX  to produce antibodies useful for diagnosis and passive immunotherapy.
XX  The purified virus may also be used in vaccines.
XX  Sequence 382 AA:
XX  Query Match 0.5%; Score 59; DB 10; Length 382;
XX  Post Local Similarity 34.5%; Pref. No. 2,200,027;
XX  Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
XX  QY 1823 VITADRE VPCITDREKAPGCTGKSGDQ 1819
XX  Db 191 VTAPQQTWPKETWAKHNNFISLQ 219
XX  RESULT 124
XX  AAG15375
XX  ID AAG15375 standard; protein; 414 AA.
XX  AC AAG15375;
XX  DI 17-OCT-2000 (first entry)
XX  DE Arabidopsis thaliana protein fragment SEQ ID NO: 15604.
XX  KW Protein identification; signal transduction pathway; metabolic pathway;
XX  biological process; gene expression; gene expression; promoter;
XX  termination sequence.
XX  Arabidopsis thaliana.
XX  EP1034405-A2.
XX  06-SEP-2000.
XX  25-SEP-2000; 2000EP-0301439.
XX  25-SEP-1999; 99US-0121825.
XX  05-MAR-1990; 99US-0133180.
XX  09-MAR-1999; 99US-0123548.
XX  23-MAR-1999; 99US-0135788.
XX  25-MAR-1999; 99US-0126264.
XX  29-MAR-1999; 99US-0126785.
XX  01-APR-1999; 99US-0127462.
XX  05-APR-1999; 99US-0128234.
XX  08-APR-1999; 99US-0128714.
XX  16-APR-1999; 99US-0129845.
XX  19-APR-1999; 99US-0130077.
XX  21-APR-1999; 99US-0130449.
XX  23-APR-1999; 99US-0130510.
XX  28-APR-1999; 99US-0130891.
XX  30-APR-1999; 99US-0131449.
XX  30-APR-1999; 99US-0132048.
XX  30-APR-1999; 99US-0132407.
XX  04-MAY-1999; 99US-0132484.
XX  05-MAY-1999; 99US-0132485.
XX  06-MAY-1999; 99US-0132486.
XX  06-MAY-1999; 99US-0132487.
XX  07-MAY-1999; 99US-0132863.
XX  11-MAY-1999; 99US-0134256.
XX  14-MAY-1999; 99US-0134218.
XX  14-MAY-1999; 99US-0134219.
XX  14-MAY-1999; 99US-0134221.
XX  14-MAY-1999; 99US-0134370.
XX  18-MAY-1999; 99US-0134768.
XX  19-MAY-1999; 99US-0134941.
XX  20-MAY-1999; 99US-0135124.
XX  21-MAY-1999; 99US-0135353.
XX  21-MAY-1999; 99US-0135629.
XX  25-MAY-1999; 99US-0136021.
XX  27-MAY-1999; 99US-0136292.
XX  28-MAY-1999; 99US-0136782.
XX  01-JUN-1999; 99US-0137033.
XX  03-JUN-1999; 99US-0137528.
XX  04-JUN-1999; 99US-0137502.
XX  07-JUN-1999; 99US-0137724.
XX  08-JUN-1999; 99US-0138094.
XX  10-JUN-1999; 99US-0138540.
XX  10-JUN-1999; 99US-0138847.
XX  14-JUN-1999; 99US-0139119.
XX  16-JUN-1999; 99US-0139452.
XX  16-JUN-1999; 99US-0139453.
XX  17-JUN-1999; 99US-0139492.
XX  18-JUN-1999; 99US-0139451.
XX  18-JUN-1999; 99US-0139455.
XX  18-JUN-1999; 99US-0139456.
XX  18-JUN-1999; 99US-0139457.
XX  18-JUN-1999; 99US-0139458.
XX  18-JUN-1999; 99US-0139459.
XX  18-JUN-1999; 99US-0139460.
XX  18-JUN-1999; 99US-0139461.
XX  18-JUN-1999; 99US-0139462.
XX  18-JUN-1999; 99US-0139463.
XX  18-JUN-1999; 99US-0139750.
XX  18-JUN-1999; 99US-0139763.
XX  21-JUN-1999; 99US-0139817.
XX  22-JUN-1999; 99US-0139899.
XX  23-JUN-1999; 99US-0140353.
XX  24-JUN-1999; 99US-0140354.
XX  24-JUN-1999; 99US-0140645.
XX  25-JUN-1999; 99US-0140823.
XX  25-JUN-1999; 99US-0140991.
XX  30-JUN-1999; 99US-0141287.
XX  01-JUL-1999; 99US-0141842.
XX  01-JUL-1999; 99US-0142154.

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100 100 amino acid sequence, esp. as immunosay products. By
101 using a fusion protein with specific affinity for early and late
102 anti-HIV antibodies, differential diagnosis of acute and chronic
103 infections may be achieved. HIV, HIV, hepatitis B virus and
104 Hepatitis C virus.
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RESULT 121
AAP90182
ID AAP90182 standard; protein; 82 AA.
XX
AC AAP90182;
XX
DT 01-MAY-1989 (first entry)
XX
DE C-terminus of superoxide dismutase (C100 fusion polypeptide).
XX
KW Hepatitis C virus; fusion polypeptide; protein; hepatitis B virus;
KW hepatitis
XX
OS Pan troglodytes.
XX
KE Key
XX Location/Qualifiers
XX Region
XX 1..9
XX Region
XX 10..14
XX Region
XX 15..377
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XX 378..382
XX
XX GN G12212511-A.
XX
XX PD 26-JUL-1989.
XX
XX PE 18-MAY-1988; 88GB-0027024.
XX
XX PR 19-MAY-1987; 8703-0122714.
XX
XX PA (CHIR) CHIRON CORPORATION.
XX
XX PI Houston, TX, China, G. Kuo G.
XX
XX WP 1989-215054/30.
XX
XX NP NPSDB; AAP90434.
XX
DE Hepatitis C virus gene - used for production of polypeptide probes.
DE polypeptide(s) and antibodies for diagnosis, prevention and
DE treatment of infection.
XX
XX DS Disclature; 114 46; 245pp; English.
XX
XX
XX The sequence is of the C-terminus of the superoxide dismutase
XX (SOD)-C100 fusion polypeptide (see AAP90434). The sequence encodes
XX antibodies which react with antibodies in patients with both A and B
XX hepatitis (NANBH). The polypeptides are used to diagnose
XX HIV-induced NANBH, to raise antibodies for immunosay of treatment,
XX or to produce vaccines. The regions show the SOD C-terminal,
XX an adaptor, the NANBH polypeptide, and an extra sequence resp.
XX
XX Sequence 82 AA:
XX
XX Query Match 0.58; Score 59; DB 10; Length 82;
XX Best Local Similarity 4.58; Fred. No. 24062;
XX Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
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XX 1 111 111 111 111
XX 191 VLLVATKRTTVALEKSWNEMHMFPESTIQ 219
XX
XX RESULT 122
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ID AAP92048 standard; protein; 82 AA.
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AC AAP92048;
XX
DT 21-JAN-1991 (first entry)
XX
DE Sequence of the carboxy-terminus of the fusion polypeptide clones of
DE hepatitis C virus (HCV).

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Query Match 0.5%; Score 59; DB 21; Length 357;

Best Local Similarity: 23.7%; Pred. No. 30.0%;
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QY 99; KSLQKGLHTLRNLLSYVSEPTLAECHAFVQVVEETAVIYGLIDPDNDAIYPTGVPEP 1049
 PS 271 GLESLTANFSLACISIKKCALATVCEZETGLIATIMPLATLPIKLTMPETZVET 729

RESULT 119

AAR23999
 ID AAR23999 standard; protein; 363 AA.

XX AAR23999;
 AC AAR23999;

DT 10-NOV-1992 (first entry)

XX Open reading frame of the hepatitis C virus C-100-3 construct.

HE Hepatitis C virus: C-100-3 construct, peptide fragment, immunoassay;
 KW reagent; probes; antibodies; HIV; HTLV; hepatitis B virus;
 KW Treponema pallidum; open reading frame.

XX Hepatitis C virus.

XX EP484787-A.

XX 13-MAY-1992.

XX 28-OCT-1991; 91EP-0118349

XX 03-NOV-1990; 90DE-4034982.

PR 19-APR-1991; 91DE-4112743.

PR 19-JUN-1991; 91DE-4120281.

PP 28-JUN-1991; 91DE-4121431

XX (BEHW) BEHRINGWERKE AG.

PA Brust S., Gerken M., Krupka U., Stuber W.

PI WP1: 1992-160606/20.

XX Peptide(s) for hepatitis-C virus detection - their use in
 immunological tests, and single test for the detection of
 different epitope(s) from different pathogens

XX Disclosure; Fig. 1; 94pp; German.

XX The sequence is a fragment of the sequence given in EP-419216.
 CC Fragments of the HCV C-100-3 construct react specifically with
 CC antibodies to hepatitis C virus. These peptides are useful as assay
 CC reagents for diagnosis of HCV infection, allowing a decrease in
 CC false positives cf. known methods. DNA sequences encoding the
 CC peptides are useful as hybridisation probes for detection and/or
 CC determin. of HCV. Antibodies raised to the peptides are useful

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PR 27-JUL-1999; 9908-0145918.
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PR 13-AUG-1999; 9908-0148684.
PR 16-AUG-1999; 9908-0149368.
PR 17-AUG-1999; 9908-0149175.
PR 18-AUG-1999; 9908-0149426.
PR 20-AUG-1999; 9908-0149722.
PR 20-AUG-1999; 9908-0149723.
PR 20-AUG-1999; 9908-0149829.
PR 23-AUG-1999; 9908-0149930.
PR 25-AUG-1999; 9908-0150566.
PR 26-AUG-1999; 9908-0150884.
PR 27-AUG-1999; 9908-0151065.
PR 27-AUG-1999; 9908-0151066.
PR 27-AUG-1999; 9908-0151080.
PR 30-AUG-1999; 9908-0151303.
PR 31-AUG-1999; 9908-0151438.
PR 01-SEP-1999; 9908-0151930.
PR 07-SEP-1999; 9908-0152363.
PR 10-SEP-1999; 9908-0153070.
PR 13-SEP-1999; 9908-0153758.
PR 15-SEP-1999; 9908-0154018.
PR 16-SEP-1999; 9908-0154039.
PR 20-SEP-1999; 9908-0154779.
PR 22-SEP-1999; 9908-0155139.

Query Match 0.5%; Score 59; DB 10; Length 117;
 Best Local Similarity 34.5%; Pred. No. 40;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPALKYKTEKLEKWNKNGPFFMSIIQ 1849
 I I I I I I I I I I I I I I I I
 Db 57 viapavqtnwqkietfwaklmwnfisiq 85

RESULT 101
 AAR13354
 ID AAR13354 standard; protein; 117 AA.

XX AAR13354

XX AAR13354

XX AAR13354

XX AAR13354

XX AAR13354

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XX AAR13354

Hepatitis C virus; NANBH; assay; antibody; p480-JH1; p480-J; p480-J2;
 p408.

XX Synthetic.

XX W09206247-A.

XX 01-APR-1993.

XX 16-SEP-1992; 92WO-US07813.

XX 16-SEP-1991; 91US-0760292

XX (ABBO) ABBOTT LAB.

XX Lesniowski RR, Leung TK;

XX WPI; 1993-117563/14.

XX Assay for detecting presence of antibody to hepatitis C viral

XX antigen - by contacting sample with polypeptide contg. at least

XX one epitope of virus antigen

XX Disclosure; Page 13; 63pp; English.

XX The synthetic peptide p1689 represents amino acid residues 1689-1805 of

XX the hepatitis C viral antigen. The peptide may be used in an assay to

XX detect antibodies to HCV and thus to diagnose chronic HCV infection.

XX See also AAR33861-87.

XX Sequence 117 AA;

Query Match 0.5%; Score 59; DB 14; Length 117;

Best Local Similarity 34.5%; Pred. No. 40;

Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPALKYKTEKLEKWNKNGPFFMSIIQ 1849

Db 57 viapavqtnwqkietfwaklmwnfisiq 85

RESULT 103

AAR13354

ID AAR13354 standard; Protein; 118 AA.

XX AAR13354

XX AAR13354

XX 23 OCT-1991 (first entry)

XX p1689 HCV antigen (1689-1805).

XX C100-3; hepatitis C virus; immunoassay; epitope.

XX Synthetic.

XX AAR13354

XX AAR13354

XX AAR13354

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XX AAR13354

Query Match 0.5%; Score 59; DB 10; Length 117;

Best Local Similarity 34.5%; Pred. No. 40;

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QY 1821 VLLPALKYKTEKLEKWNKNGPFFMSIIQ 1849

Db 57 viapavqtnwqkietfwaklmwnfisiq 85

RESULT 102

AAR13372

ID AAR13372 standard; peptide; 117 AA.

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

XX AAR13372

Immunological assays for hepatitis C virus antibody - by using
 polypeptide(s) contg. epitope(s) of hepatitis C virus antigens
 Claim 1; Page 45; 62pp; English.

of immunity. The attenuated bacterium retains sufficient virulence to cause infection in the virulent organism and this is a good immunogen.

Supply 127 AA:

Query Match:	0.96	Score: 478	IP: 122	Length: 4,237
Best Local Similarity:	47.8%	Prod. No.: 13900-22		
Motif:	11	Conservation:	4	Differences: 10
CY 2028 ENR100KKEGVFKHLPQTA 2050				
1 1111 : 1111 : 1111 :				
DE 112 CYMLQSPFMEETMIMVGLD 134				

Query Match: 0.68; Score for: 108.17; Length: 4.97;
Best local similarity: 43.08; Freq. Mod.: 4.42;
Matches: 14; 0.058-negative; 6. Mismatch: 3; 1% identity

[illegible]

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Gender	1.0	0.0	1	1
Marital status	1.0	0.0	1	1
Education	14.0	2.0	10	18
Income	1.0	0.0	1	1
Religion	1.0	0.0	1	1
Occupation	1.0	0.0	1	1
Health	1.0	0.0	1	1
Smoking	1.0	0.0	1	1
Alcohol	1.0	0.0	1	1
Exercise	1.0	0.0	1	1
Stress	1.0	0.0	1	1
Depression	1.0	0.0	1	1
Loneliness	1.0	0.0	1	1
Life satisfaction	1.0	0.0	1	1
Quality of life	1.0	0.0	1	1
Overall health	1.0	0.0	1	1
Physical health	1.0	0.0	1	1
Mental health	1.0	0.0	1	1
Social health	1.0	0.0	1	1
Emotional health	1.0	0.0	1	1
Behavioral health	1.0	0.0	1	1
Environmental health	1.0	0.0	1	1
Healthcare access	1.0	0.0	1	1
Healthcare quality	1.0	0.0	1	1
Healthcare cost	1.0	0.0	1	1
Healthcare coverage	1.0	0.0	1	1
Healthcare utilization	1.0	0.0	1	1
Healthcare satisfaction	1.0	0.0	1	1
Healthcare equity	1.0	0.0	1	1
Healthcare innovation	1.0	0.0	1	1
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Healthcare governance	1.0	0.0	1	1
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Healthcare mission	1.0	0.0	1	1
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Healthcare climate	1.0	0.0	1	1
Healthcare environment	1.0	0.0	1	1
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Healthcare knowledge	1.0	0.0	1	1
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Healthcare wisdom	1.0	0.0	1	1
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Healthcare modesty	1.0	0.0	1	1
Healthcare simplicity	1.0	0.0	1	1
Healthcare clarity	1.0	0.0	1	1
Healthcare transparency	1.0	0.0	1	1
Healthcare honesty	1.0	0.0	1	1
Healthcare integrity	1.0	0.0	1	1
Healthcare trustworthiness	1.0			

[illegible]

AAPI Press, 3001 1st St., Berkeley, CA 94701

Accepted and registered for printing 20 April 1987

in an effort to understand the mechanism of the fishery, the disease was considered in the light of its development in part of the aromatic hydrocarbon pathway in *Aeromonas salmonicida*. It is very similar to several fish-pathogenic mutations in the aromatic hydrocarbon pathway in *Escherichia coli* and *Serratia marcescens*. But mutants in the aromatic hydrocarbon pathway could be used in the fish, on vaccines for fish, on the same salmon or trout, for the prevention of bacterial infection. The mutants are available, suitable for prevention of bacterial infection in fish and stimulate protective response up to 2 weeks in infected fish and stimulate protective response up to 2 weeks in vaccinated fish. The fishery system is described in the following.

PR	28-SEP-1999	990S-0156458.	PR	29-MAR-1999	990S-0126785.
PR	29-SEP-1999	990S-0156596.	PR	01-APR-1999	990S-0127462.
PR	05-OCT-1999	990S-0157117.	PR	06-APR-1999	990S-0128234.
PR	05-OCT-1999	990S-0157553.	PR	08-APR-1999	990S-0128714.
PR	06-OCT-1999	990S-0157865.	PR	09-APR-1999	990S-0129845.
PR	07-OCT-1999	990S-0158029.	PR	19-APR-1999	990S-0130077.
PR	08-OCT-1999	990S-0158232.	PR	21-APR-1999	990S-0130449.
PR	12-OCT-1999	990S-0158369.	PR	23-APR-1999	990S-0130510.
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Best Local Similarity: 28.59; Field No. 130602;

Mismatches 14; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

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DB 212 KQTHSEKFNVAAGVACDSEMSQTHHHAHLLHLLHVACTHPPVHNI 1303

RESULT 83

AA021584

AA021584 standard; Protein; 348 AA.

XX AA021584;

XX AA021584;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment 302 to 303, 24193.

XX protein in Arabidopsis thaliana, signal transduction pathway, metabolic pathway,

XX hybridisation assay; quantitative; non-expression control; fragment,

XX termination sequence.

XX Arabidopsis thaliana.

XX EP103405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP 090149.

XX 25-FEB-1999; 990S-0121825.

XX 05-MAR-1999; 990S-0124180.

XX 09-MAR-1999; 990S-0123548.

XX 23-MAR-1999; 990S-0125788.

XX 25-MAR-1999; 990S-0125264.

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hybridization assay; genetic mapping; gene expression control; promoter;
termination sequence.
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OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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KW Protein identification, signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
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 PR 09-AUG-1999; 990S-0147935.
 PR 10-AUG-1999; 990S-0148171.
 PR 11-AUG-1999; 990S-0148319.
 PR 12-AUG-1999; 990S-0148341.
 PR 13-AUG-1999; 990S-0148565.
 PR 13-AUG-1999; 990S-0148684.
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 PR 17-AUG-1999; 990S-0149175.
 PR 18-AUG-1999; 990S-0149426.
 PR 20-AUG-1999; 990S-0149722.
 PR 20-AUG-1999; 990S-0149723.
 PR 20-AUG-1999; 990S-0149929.
 PR 23-AUG-1999; 990S-0149902.
 PR 23-AUG-1999; 990S-0149930.

PR 25-AUG-1999; 990S-0150566.
 PR 26-AUG-1999; 990S-0150884.
 PR 27-AUG-1999; 990S-0151065.
 PR 27-AUG-1999; 990S-0151066.
 PR 27-AUG-1999; 990S-0151080.
 PR 30-AUG-1999; 990S-0151303.
 PR 31-AUG-1999; 990S-0151438.
 PR 01-SEP-1999; 990S-0151930.
 PR 07-SEP-1999; 990S-0152363.
 PR 10-SEP-1999; 990S-0153070.
 PR 13-SEP-1999; 990S-0153758.
 PR 15-SEP-1999; 990S-0154018.
 PR 16-SEP-1999; 990S-0154039.
 PR 20-SEP-1999; 990S-0154779.
 PR 22-SEP-1999; 990S-0155139.
 PR 23-SEP-1999; 990S-0155486.
 PR 24-SEP-1999; 990S-0155659.
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 PR 29-SEP-1999; 990S-0156596.
 PR 04-OCT-1999; 990S-0157117.
 PR 05-OCT-1999; 990S-0157553.
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 PR 18-OCT-1999; 990S-0159584.
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 PR 21-OCT-1999; 990S-0160814.
 PR 21-OCT-1999; 990S-0160815.
 PR 22-OCT-1999; 990S-0160980.
 PR 22-OCT-1999; 990S-0160981.
 PR 22-OCT-1999; 990S-0160989.
 PR 25-OCT-1999; 990S-0161404.
 PR 25-OCT-1999; 990S-0161405.
 PR 25-OCT-1999; 990S-0161406.
 PR 26-OCT-1999; 990S-0161359.
 PR 26-OCT-1999; 990S-0161360.
 PR 26-OCT-1999; 990S-0161361.
 PR 28-OCT-1999; 990S-0161920.
 PR 28-OCT-1999; 990S-0161992.
 PR 28-OCT-1999; 990S-0161993.
 PR 29-OCT-1999; 990S-0162142.

Query Match 0.6%; Score 61; DR 21; Length 357;
 Best Local Similarity 42.4%; Prod. No. 111c-02;
 Matches 14; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1631 ISMKKTIVIRKLVDPDLAIYORKKKKGHEQ 1663
 Db 316 ldykraiatttphlllpllllreslperceee 318

RESULT 71
 AAG18559
 ID AAG18559 standard; Protein; 369 AA.
 XX AAG18559;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 20017.
 XX

PR	17 AUG 1999	9908-014025	XX	AA04-0089;
PR	18 AUG 1999	9908-014026	XX	
PR	20 AUG 1999	9908-014027	XX	18 OCT-2000 (first entry)
PR	21 AUG 1999	9908-014028	XX	
PR	23 AUG 1999	9908-014029	XX	Arabidopsis thaliana protein fragment SEQ ID NO: 6005.
PR	25 AUG 1999	9908-014030	XX	Protein identification: signal transduction pathway; mutated in pathway;
PR	26 AUG 1999	9908-014031	XX	hybridisation assay; detected in map; not detected in control; Promoter;
PR	27 AUG 1999	9908-014032	XX	termination sequence.
PR	28 AUG 1999	9908-014033	XX	
PR	29 AUG 1999	9908-014034	XX	Arabidopsis thaliana.
PR	30 AUG 1999	9908-014035	XX	FF1043405-AZ.
PR	31 AUG 1999	9908-014036	XX	06-SEP-2000.
PR	32 AUG 1999	9908-014037	XX	
PR	33 AUG 1999	9908-014038	XX	25 FEB-2000; 2000EP-0401439.
PR	34 AUG 1999	9908-014039	XX	
PR	35 AUG 1999	9908-014040	XX	25-FEB-1999; 9908-0121825.
PR	36 AUG 1999	9908-014041	XX	05-MAR-1999; 9908-0124380.
PR	37 AUG 1999	9908-014042	XX	09-MAR-1999; 9908-0124548.
PR	38 AUG 1999	9908-014043	XX	24-MAR-1999; 9908-0125788.
PR	39 AUG 1999	9908-014044	XX	25-MAR-1999; 9908-012624.
PR	40 AUG 1999	9908-014045	XX	29-MAR-1999; 9908-0126765.
PR	41 AUG 1999	9908-014046	XX	01-APR-1999; 9908-0127462.
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PR	44 AUG 1999	9908-014049	XX	16-APR-1999; 9908-0129845.
PR	45 AUG 1999	9908-014050	XX	19-APR-1999; 9908-0130077.
PR	46 AUG 1999	9908-014051	XX	21-APR-1999; 9908-0130419.
PR	47 AUG 1999	9908-014052	XX	24-APR-1999; 9908-0130510.
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PR	49 AUG 1999	9908-014054	XX	30-APR-1999; 9908-0131349.
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PR	52 AUG 1999	9908-014057	XX	08-MAY-1999; 9908-0132484.
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PR	54 AUG 1999	9908-014059	XX	06-MAY-1999; 9908-0132486.
PR	55 AUG 1999	9908-014060	XX	07-MAY-1999; 9908-0132487.
PR	56 AUG 1999	9908-014061	XX	07-MAY-1999; 9908-0132864.
PR	57 AUG 1999	9908-014062	XX	11-MAY-1999; 9908-0134256.
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PR	59 AUG 1999	9908-014064	XX	14-MAY-1999; 9908-0134219.
PR	60 AUG 1999	9908-014065	XX	14-MAY-1999; 9908-0134221.
PR	61 AUG 1999	9908-014066	XX	14-MAY-1999; 9908-0134370.
PR	62 AUG 1999	9908-014067	XX	18-MAY-1999; 9908-0134768.
PR	63 AUG 1999	9908-014068	XX	19-MAY-1999; 9908-0134941.
PR	64 AUG 1999	9908-014069	XX	20-MAY-1999; 9908-0135124.
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PR	67 AUG 1999	9908-014072	XX	25-MAY-1999; 9908-0136021.
PR	68 AUG 1999	9908-014073	XX	27-MAY-1999; 9908-0136492.
PR	69 AUG 1999	9908-014074	XX	28-MAY-1999; 9908-0136782.
PR	70 AUG 1999	9908-014075	XX	01-JUN-1999; 9908-0137222.
PR	71 AUG 1999	9908-014076	XX	04-JUN-1999; 9908-0137528.
PR	72 AUG 1999	9908-014077	XX	04-JUN-1999; 9908-0137502.
PR	73 AUG 1999	9908-014078	XX	07-JUN-1999; 9908-0137744.
PR	74 AUG 1999	9908-014079	XX	08-JUN-1999; 9908-0138094.
PR	75 AUG 1999	9908-014080	XX	10-JUN-1999; 9908-0138540.
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PR	78 AUG 1999	9908-014083	XX	16-JUN-1999; 9908-0139453.
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PR	81 AUG 1999	9908-014086	XX	18-JUN-1999; 9908-0139455.
PR	82 AUG 1999	9908-014087	XX	18-JUN-1999; 9908-0139456.
PR	83 AUG 1999	9908-014088	XX	18-JUN-1999; 9908-0139457.
PR	84 AUG 1999	9908-014089	XX	18-JUN-1999; 9908-0139458.
PR	85 AUG 1999	9908-014090	XX	18-JUN-1999; 9908-0139459.
PR	86 AUG 1999	9908-014091	XX	18-JUN-1999; 9908-0139460.
PR	87 AUG 1999	9908-014092	XX	18-JUN-1999; 9908-0139461.

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2000 MAR 09 10:00 Source: 13; Zip: 21; Length: 463;

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PR 04-AUG-1999; 990S-0147302.
PR 05-AUG-1999; 990S-0147192.
PR 05-AUG-1999; 990S-0147260.
PR 06-AUG-1999; 990S-0147303.
PR 06-AUG-1999; 990S-0147416.
PR 09-AUG-1999; 990S-0147493.
PR 09-AUG-1999; 990S-0147535.
PR 10-AUG-1999; 990S-0148171.
PR 11-AUG-1999; 990S-0148319.
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PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149175.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
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PR 23-AUG-1999; 990S-0149940.
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PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 30-AUG-1999; 990S-0151303.
PR 31-AUG-1999; 990S-0151448.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152463.
PR 10-SEP-1999; 990S-0153070.
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PR 26-SEP-1999; 990S-0156536.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.
PR 06-OCT-1999; 990S-0157865.
PR 07-OCT-1999; 990S-0158029.
PR 08-OCT-1999; 990S-0158232.
PR 12-OCT-1999; 990S-0158369.
PR 13-OCT-1999; 990S-0159293.
PR 13-OCT-1999; 990S-0159294.
PR 13-OCT-1999; 990S-0159329.
PR 14-OCT-1999; 990S-0159339.
PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159784.
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PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 25-OCT-1999; 990S-0161407.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161922.
PR 28-OCT-1999; 990S-0161993.

PR 29-OCT-1999; 990S-0162142.

Query Match: 0 68; Score 61; DB 21; Length 152;
Best Local Similarity 42.48; Pred. NO. 1e+02;
Matches 14; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1631 ISWKKTIIVTPELKLVPDLIAIVQPKKKKEEFQ 1663
Db 311 IYKrgIvYtqkIprIltavresIvKvKvKvKv 343

RESULT 68
AAG49090
ID AAG49090 standard; Protein; 352 AA.
XX
AC AAG49090;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62066.
XX
KW Protein identification, signal transduction pathway, metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000
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PE 25-FEB-2000; 2000FP-0301439.
XX
PE 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-012180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
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PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
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PR 05-MAY-1999; 990S-0132484.
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PR 06-MAY-1999; 990S-0132486.
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PR 07-MAY-1999; 990S-0132863.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
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PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
```


CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, anoxogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
 CC ocular disorders e.g. corneal infection. The polypeptides can also be
 CC used to aid wound healing and epithelial cell proliferation, to prevent
 CC skin aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotherapy. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities, fat content,
 CC lipid, protein, carbohydrate, vitamins, minerals, cofactors and other
 CC nutritional components. AAF22297 to AAF22415 and AAB62048 represent
 CC sequences used in the exemplification of the present invention.

XX
 SQ Sequence 226 AA;

Query Match 0.6%; Score 62; DB 21; Length 226;
 Best Local Similarity 41.7%; Pred. No. 40;
 Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 919 VVTSLLINLGSPVKVRPAATGCTGALSCVASPPFYI 954
 ||| | | | | | | | | | | | | | | |
 DB 155 VTKILNLSPPSMARVIAALQMBALTRIPYVLL 190

RESULT 60

AAAY67644
 ID AAY67644 standard; Protein; 241 AA.

XX
 AC AAY67644;

XX
 DI 07-OCT-1999 (first entry)

XX
 DE Protein which is specific to Chlamydia trachomatis.

XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritrichitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis.

XX
 OS Chlamydia trachomatis.

XX
 PN W09428475-A2.

XX
 PD 10-JUN-1999.

XX
 PF 27-NOV-1998; 98WG 1B01939.

XX
 PP 04-NOV-1998; 98GS 0107077.

XX
 PR 28-NOV-1997; 97ER-0015041.

XX
 PR 17-DEC-1997; 97ER-0016034.

XX
 PA (GST) GENSET.

XX
 PI Griffiths R;

XX
 PR WFL 1999 171125/31.

XX
 PI Genome sequence of Chlamydia trachomatis

XX
 PS Disclosure, Page 1273, 1755pp; English.

XX
 CC AAY67644 (3795) are encoded by open reading frames (ORFs) of the genome
 CC of Chlamydia trachomatis (see AAF01425). The polypeptides can be used as
 CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis, genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC peritrichitis, Bartholinitis, pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the invention
 CC may be of use in treating these diseases.

XX
 SQ Sequence 234 AA;

Query Match 0.6%; Score 62; DB 20; Length 234;
 Best Local Similarity 42.9%; Pred. No. 42;
 Matches 12; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1018 LMKVLQGVNCRMVLSQLPMAHQHLEKI 1045

||| | | | | | | | | | | | | | | |
 DB 72 LMDLQGLSGLLQGLGLSDVLEEL 99

RESULT 61

AAB61304
 ID AAB61304 standard; Protein; 615 AA.

XX
 AC AAB61304;

XX
 DI 30-MAR-2001 (first entry)

XX
 DE Human transcriptional regulator protein #4.

XX
 KW Human; transcriptional regulator protein; IXPEG.

XX
 OS Homo sapiens.

XX
 PN W0200079954-A2.

XX
 PD 29-DEC-2000.

XX
 PF 15-JUN-2000; 2000WO-0516766

XX
 PR 18-JUN-1999; 99US-0140109.

XX
 PA (INCY) INCYTE GEN-MICS INC.

XX
 PI Lal P, Yue H, Tang YT, Baughn ME, Azimzal Y, Tran B;

XX
 DR WPI; 2001-041425/05.

XX
 PT Isolated polypeptide with a human transcriptional regulator protein
 PT sequence is useful for the diagnosis, prevention and treatment of
 PT disorders associated with the immune, reproductive and cardiovascular
 PT systems -

XX
 PS Claim 1; Page 95-96; 142pp; English.

XX
 CC The present invention relates to human transcriptional regulator
 CC protein (IXPEG) sequences. The antagonist and an agonist of the proteins
 CC of the invention are used to treat disorders associated with decreased
 CC or increased expression of activity of IXPEG.

XX
 SQ Sequence 615 AA;

Query Match 0.6%; Score 62; DB 22; Length 615;
 Best Local Similarity 41.7%; Pred. No. 1,7e+02;
 Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 919 VVTSLLINLGSPVKVRPAATGCTGALSCVASPPFYI 954

DB 540 VTKILNLSPPSMARVIAALQMBALTRIPYVLL 575

RESULT 62

AAAY69294
 ID AAY69294 standard; Protein; 701 AA.

XX
 AC AAY69294;

XX
 DI 19-JUN-2000 (first entry)

XX

11 used to produce a functional active protein
 XX Chain 34; Page 1; 24pp; English
 XX
 12 This protein sequence is as the sequence given in AAF2002 except
 13 that Ala at position 46 is replaced by Val.
 14 This protein specifically binds to the enhancer of the alpha-
 15 fetoprotein gene. The DNA encoding this protein may be useful for
 16 an expression vector and for transfection into animal cells with another
 17 expression vector in which a gene for the biologically active protein
 18 is placed under the control of alpha-fetoprotein gene enhancer and
 19 promoter.
 XX Sequence: 276 AA;
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01 of protein content (e.g., 2 to 5-fold increase) and higher levels of
 02 essential amino acids. The present sequence represents a specifically
 03 claimed PDPI tetrameric protein from the present invention.
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 04 Sequence: 172 AA;
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Query Match
Best local similarity 28.3% (Prod. No. 1266-24)
Matches 15 Conservative 10 Mismatches 40 Indels 0 Gaps 0

27 69 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 129
28 205 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 47

RESULT 95
AAW44621
10 AAW44621 standard; Protein: 1266 AA

XX Key location/qualifiers
XX Domain 1231..1291
XX Note "homodomain"
XX Domain 1328..1388
XX Label homodomain
XX Domain 1727..1786
XX Label homodomain
XX Domain 2032..2091

Query Match
Best local similarity 28.3% (Prod. No. 1266-24)
Matches 15 Conservative 10 Mismatches 40 Indels 0 Gaps 0

27 69 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 129
28 205 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 47

RESULT 95
AAW44621
10 AAW44621 standard; Protein: 1266 AA

Query Match
Best local similarity 28.3% (Prod. No. 1266-24)
Matches 15 Conservative 10 Mismatches 40 Indels 0 Gaps 0

27 69 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 129
28 205 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 47

RESULT 95
AAW44621
10 AAW44621 standard; Protein: 1266 AA

XX Key location/qualifiers
XX Domain 1231..1291
XX Note "homodomain"
XX Domain 1328..1388
XX Label homodomain
XX Domain 1727..1786
XX Label homodomain
XX Domain 2032..2091

Query Match
Best local similarity 28.3% (Prod. No. 1266-24)
Matches 15 Conservative 10 Mismatches 40 Indels 0 Gaps 0

27 69 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 129
28 205 PPSGLAVLPPVETKAVNKEQENINSEIFLHSPVLEKFAKQLEWLEHR 47

RESULT 95
AAW44621
10 AAW44621 standard; Protein: 1266 AA

XX Key location/qualifiers
XX Domain 1231..1291
XX Note "homodomain"
XX Domain 1328..1388
XX Label homodomain
XX Domain 1727..1786
XX Label homodomain
XX Domain 2032..2091

A1 AAY22471
 XX 29-SEP-1999 (first entry)
 XX Human hippocampus; Alzheimer's disease; PS 1; PS 2: hippocampus;
 XX first entry.
 KW Sol-10 human protein; Alzheimer's disease; PS 1; PS 2: hippocampus;
 KW first entry.
 XX amino acid sequence
 XX W09932623-A1
 XX 01-JUL-1999
 XX 17-DEC-1998; 98WO-US26820.
 XX 19-SEP-1999; 97US-0068243.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Gurney ME, Li J, Pauley AM;
 XX WPI: 1999-458026/18.
 XX N-USDB; AAX99716.
 XX New isolated human sol-10 polypeptides
 XX Claim 1: Page 60-64; 116pp; English.
 XX the present invention relates to human sol-10. The sol-10 proteins of
 XX the invention are useful for raising monoclonal or polyclonal
 XX antibodies useful in diagnostic assays for detecting sol-10
 XX polypeptide expression. The sol-10 polypeptides are also useful as drug
 XX targets for decreasing antibody levels in the treatment of Alzheimer's
 XX disease. It is also useful for identifying agents capable of
 XX altering the production level of Abeta. The polypeptides are useful
 XX for developing assays for identifying agents capable of interfering
 XX with the biological pathways that lead to Alzheimer's disease.
 XX Sequence 627 AA;
 SQ
 Query Match 0.68; score 64; DR 22; Length 627;
 Best local Similarity 27.5%; Pred. No. 94;
 Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;
 Q7 50 GLEHLLGLDPSFDFEAVLSGLAKLLESVSKAVKGLLENISLEHLSYFELKRP 109
 D6 165 APEKLLHLLKLDLSEKPTKPKKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 224
 Q7 110 AKKLEWLI 116
 D6 225 APTQYWR 233
 RESULT 47
 AAY22471
 10 AAY22471 standard; Protein; 666 AA.
 XX AAY22471;
 XX 29-SEP-1999 (first entry)
 XX Human C-term myelin tagged sol-10 protein sequence.
 XX Sol-10; human; presenilin; Alzheimer's disease; PS 1; PS 2: hippocampus;
 XX therapy; mammary gland.
 XX Homo sapiens.
 XX Synthetic.
 XX W09932623-A1.
 XX 01-JUL-1999.
 XX 17-DEC-1998; 98WO-US26820.
 XX 19-SEP-1999; 97US-0068243.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Gurney ME, Li J, Pauley AM;
 XX WPI: 1999-458026/18.
 XX N-USDB; AAX99716.

XX 29-SEP-1999; 99US-0428877.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Pauley AM, Gurney ME, Li J;
 XX WPI: 2001-102404/11.
 XX New human sol-10 polypeptides and their encoding polynucleotides,
 XX useful for raising antibodies for detecting sol-10 polypeptide
 XX expression and as drug targets in the treatment of Alzheimer's disease.
 XX Claim 1: Page 60-64; 116pp; English.
 XX the present invention relates to human sol-10. The sol-10 proteins of
 XX the invention are useful for raising monoclonal or polyclonal
 XX antibodies useful in diagnostic assays for detecting sol-10
 XX polypeptide expression. The sol-10 polypeptides are also useful as drug
 XX targets for decreasing antibody levels in the treatment of Alzheimer's
 XX disease. It is also useful for identifying agents capable of
 XX altering the production level of Abeta. The polynucleotides are useful
 XX for developing assays for identifying agents capable of interfering
 XX with the biological pathways that lead to Alzheimer's disease.
 XX Sequence 627 AA;
 SQ
 Query Match 0.68; score 64; DR 22; Length 627;
 Best local Similarity 27.5%; Pred. No. 94;
 Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;
 Q7 50 GLEHLLGLDPSFDFEAVLSGLAKLLESVSKAVKGLLENISLEHLSYFELKRP 109
 D6 165 APEKLLHLLKLDLSEKPTKPKKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 224
 Q7 110 AKKLEWLI 116
 D6 225 APTQYWR 233
 RESULT 47
 AAY22471
 10 AAY22471 standard; Protein; 666 AA.
 XX AAY22471;
 XX 29-SEP-1999 (first entry)
 XX Human C-term myelin tagged sol-10 protein sequence.
 XX Sol-10; human; presenilin; Alzheimer's disease; PS 1; PS 2: hippocampus;
 XX therapy; mammary gland.
 XX Homo sapiens.
 XX Synthetic.
 XX W09932623-A1.
 XX 01-JUL-1999.
 XX 17-DEC-1998; 98WO-US26820.
 XX 19-SEP-1999; 97US-0068243.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Gurney ME, Li J, Pauley AM;
 XX WPI: 1999-458026/18.
 XX N-USDB; AAX99716.


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RESULT 38
AAB01204
ID AAB01204 standard; protein; 589 AA.
XX
AC AAB01204;
XX
DT 03-NOV-2000 (first entry)
XX
DE Human GTPase associated protein-29.
XX
OS Homo sapiens.
FW Guanine nucleotide binding protein; GTP binding protein, G-protein;
KW GTPase; GTPase associated protein; GTPAP; cell proliferation;
KW autoimmune, inflammatory, immune system disorder, cancer, AIDS,
KW acquired immune deficiency syndrome; asthma; atherosclerosis;
KW arthritis; systemic lupus erythematosus, psoriasis, human.
XX
OS Homo sapiens.
FW W2000031263 A2.
XX
PR 02-JUN-2000.
XX
DT 23-NOV-1999; 99WO-US28013.
XX
PR 23 NOV 1999; 98US-0105592.
XX
PR 04-FEB-1999; 99US-0118610.
XX
PR 06-APR-1999; 99US-0127990
XX
PA (INCYTE) INCYTE PHARM INC.
XX
PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;
PI Yang J, Azimzai Y;
XX
DR WPI; 2000-400073/34.
XX
DR N-PSDB; AAA49159.
XX
PT Human GTPase associated proteins, polynucleotides, and antibodies,
PT useful for diagnosing, preventing and treating various diseases such as
PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
PT asthma, and autoimmune diseases -
XX
PS Claim 1, Page 118 120, 144pp, English.
XX
CC Human cDNA libraries from various tissues were screened for GTPase
CC associated proteins (GTPAP). The present sequence is human
CC GTPAP-29 protein. This sequence was derived from a cDNA library of
CC brain tumor tissue. This protein is expressed in nervous,
CC reproductive and gastrointestinal tissue. The GTPAP proteins may be
CC used to define agonists and antagonists of GTPAP activity and to
CC generate antibodies to GTPAP. This means the GTPAP proteins may be
CC useful for treatment or prevention of diseases associated with GTPAP
CC such as cell proliferation disorders, autoimmune disorders,
CC inflammatory disorders, immune system disorders, cancer, AIDS, asthma,
CC atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis.
XX
SQ Sequence 589 AA;

Query Match 0.68; Score 64; DP 21; Length 589;
Best Local Similarity 27.5%; Pred. No. 86;
Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 50 TGLEELGLGDPSEQFEAPLESGLAKTLERSVOTKAVNKQLDENISLFTIHLSPTVFLKPP 109
DB 127 sqpeklalidelidsceptqvlummdvlepfqfrdiisilpkelalylvlsflepklbqa 186
QY 110 AOKCLEWLI 118
DB 187 agtcrwyri 195

RESULT 39
AAB59198
ID AAB59198 standard; protein; 589 AA.
XX
AC AAB59198;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human mammary sel-10-1 protein.
XX
KW Sel-10; human; Alzheimer's disease; Abeta.
XX
OS Homo sapiens.
FW W0200075448-A1
XX
PR 14-SEP-2000.
XX
DT 23-MAY-2000; 2000WO-US09814
XX
PR 09-JUN-1999; 99US-0328877.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Pauley AM, Gurney ME, Li J;
XX
PR WPI; 2001-102404/11.
XX
PT New human sel-10 polypeptides and their encoding polynucleotides,
PT useful for raising antibodies for detecting sel 10 polypeptide
PT expression and as drug targets in the treatment of Alzheimer's disease
XX
PS Claim 1; Page 79-82; 116pp; English.
XX
CC The present invention relates to human sel-10. The sel 10 proteins of
CC the invention are useful for raising monoclonal or polyclonal
CC antibodies useful in diagnostic assays for detecting sel-10
CC polypeptide expression. The sel-10 polypeptides are also useful as drug
CC targets for decreasing antibody levels in the treatment of Alzheimer's
CC disease. It is also useful for identifying agents capable of
CC altering the production level of Abeta. The polynucleotides are useful
CC for developing assays for identifying agents capable of interfering
CC with the biological pathways that lead to Alzheimer's disease.
XX
SQ Sequence 589 AA;

Query Match 0.68; Score 64; DP 22; Length 589;
Best Local Similarity 27.5%; Pred. No. 86;
Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 50 TGLEELGLGDPSEQFEAPLESGLAKTLERSVOTKAVNKQLDENISLFTIHLSPTVFLKPP 109
DB 127 sqpeklalidelidsceptqvlummdvlepfqfrdiisilpkelalylvlsflepklbqa 186
QY 110 AOKCLEWLI 118
DB 187 agtcrwyri 195

RESULT 40
AAY22462
ID AAY22462 standard; protein; 592 AA.
XX
AC AAY22462;
XX
DT 29-SEP-1999 (first entry)
XX
DE Human hippocampal sel-10 protein sequence.
XX
KW Sel-10; human, presenilin, Alzheimer's disease; PS-1; PS-2; hippocampus;
KW therapy.

```


the invention are useful for raised monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta, the polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.

XX Sequence 540 AA;

Query Match 0.6%; Score 64; DB 22; Length 540;

Best Local Similarity 27.5%; Pred. No. 76;

Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 50 TGLLELLCHLHSEFPEAFESLSEAFLEPVSQTPAVNPGLHNNISLHLSVLELKP 109
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 QY 110 AOKGLEWLI 118
 DB 143 aqerywri 146

RESULT 31

AAAY22464

XX AAAY22464 standard; protein; 545 AA.

XX AAAY22464;

XX 20-SEP-1999 (first entry)

XX Human hippocampal sel-10 protein sequence.

XX Sel-10; human; presenilin Alzheimer's disease; PS-1; PS-2; hippocampus; therapy.

XX Homo sapiens.

XX W0200075428-A1.

XX 01-JUN-1999.

XX 10-DEC-1998; 98W00US26820.

XX 10-DEC-1998; 97US0068215.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gurney ME, Li J, Pauley AM;

XX WPI; 1999-456928/06.

XX NLSUB: AAX00701.

XX New isolated human sel-10 polypeptides

XX claim 24; Page 54-56; 91pp; English.

XX This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human hippocampal sel-10 protein. The polypeptides can be used to alter presenilin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presenilin-1 (PS-1) or PS-2, and thereby be useful for the prevention or treatment of Alzheimer's disease.

XX Sequence 545 AA;

Query Match 0.6%; Score 64; DB 20; Length 545;

Best Local Similarity 27.5%; Pred. No. 76;

Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 50 TGLLELLCHLHSEFPEAFESLSEAFLEPVSQTPAVNPGLHNNISLHLSVLELKP 109
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 QY 110 AOKGLEWLI 118
 DB 143 aqerywri 151

RESULT 32

AAAB59196

XX AAAB59196 standard; protein; 545 AA.

XX AAAB59196;

XX 23-MAR-2001 (first entry)

XX Human hippocampal sel-10-4 protein.

XX Sel-10; human; Alzheimer's disease; Abeta.

XX Homo sapiens.

XX W0200075428-A1.

XX 14-DEC-2000.

XX 23-MAY-2000; 2000W00US09814.

XX 09-JUN-1999; 99US-0328877.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Pauley AM, Gurney ME, Li J;

XX WPI; 2001 102404/11.

XX New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease.

XX claim 1; Page 72-75; 116pp; English.

XX The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta, the polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.

XX Sequence 545 AA;

Query Match

Best Local Similarity 27.5%; Score 64; DB 22; Length 545;

Matches 19; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

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QY 110 AOKGLEWLI 118

DB 143 aqerywri 151

RESULT 33

AAAY22463

XX AAAG-766.
XX 16 JUL 2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 76748.
XX protein fragment: signal: fused action pathway; metabolic pathway;
KW hydrolysis assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EPI 34 5, A2.
XX 06 SEP 2000.
XX 25 FEB 2000 2000EP-0001434.
XX 25 FEB 1999 990S-012925.
XX 01 MAR 1999 990S-012960.
XX 09 MAR 1999 990S-012948.
XX 23 MAR 1999 990S-012578.
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XX 29 MAR 1999 990S-012675.
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XX 6 APR 1999 990S-012624.
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Query Match 0.6%; Score 64; DR 21; Length 109;
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XX OS Neisseria gonorrhoeae.
XX PN WC9924578-A2.
XX XX
XX PD 20-MAY-1999.
XX PF 09-OCT-1998; 98WO-1801665.
XX PR 01-SEP-1998; 98GB-0019016.
XX PR 06-NOV-1997; 97GB-0023516.
XX PR 14-NOV-1997; 97GB-0024190.
XX PR 18-NOV-1997; 97GB-0024386.
XX PR 27-NOV-1997; 97GB-0025158.
XX PR 10-DEC-1997; 97GB-0026147.
XX PR 14-JAN-1998; 98GB-0000759.
XX PA (CHIR-) CHIRON SPA.
XX PI Grandi G, Masiagnani V, Piazza M, Rappuoli R, Scarlato V;
XX XX
XX WPI; 1999-327407/27.
XX PR P-PSDB; AAY38789.
XX PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX PT diagnosis, treatment and prevention of infection
XX PS Claim 4; Page 332; 524pp; English.
XX SQ Sequence 513 AA;

CC Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
CC and N. gonorrhoeae antigenic proteins. They are encoded by open
CC reading frames (ORFs) AAC11972-212358. The antigenic proteins,
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of Neisseria
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX SQ Sequence 513 AA;

Query Match 0.68; Score 67; DB 20; Length 513;
Best local Similarity 44.79; Pred. No. 27;
Matches 17; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Q7 184 KDLGPMDFICSLVTKSVKVFVAFETFGSSAQLRLVLAIFYA 221
: | | | | | | | | | | | | | | | | | | |
Db 349 rglvflpfmvsprvcsagvlllypgwtasipillamy 386

RESULT 6
AAY38789
ID AAY38789 standard; Protein: 513 AA.
XX AC AAY38789;
XX DT 08-OCT-1999 (first entry)
XX DE Neisseria gonorrhoeae antigenic protein encoded by ORF139.
XX KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX OS Neisseria gonorrhoeae.
XX PN WC9924578-A2.
XX PD 20-MAY-1999.
XX PF 09-OCT-1998; 98WO-1801665.
XX PR 01-SEP-1998; 98GB-0019016.
XX PR 06-NOV-1997; 97GB-0023516.

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PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX PA (CHIR-) CHIRON SPA.
XX PI Grandi G, Masiagnani V, Piazza M, Rappuoli R, Scarlato V;
XX XX
XX WPI; 1999-327407/27.
XX PR P-PSDB; AAY38789.
XX PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX PT diagnosis, treatment and prevention of infection
XX PS Claim 4; Page 332; 524pp; English.
XX SQ Sequence 513 AA;

CC Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
CC and N. gonorrhoeae antigenic proteins. They are encoded by open
CC reading frames (ORFs) AAC11972-212358. The antigenic proteins,
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of Neisseria
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX SQ Sequence 513 AA;

Query Match 0.68; Score 67; DB 20; Length 513;
Best local Similarity 44.79; Pred. No. 27;
Matches 17; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Q7 184 KDLGPMDFICSLVTKSVKVFVAFETFGSSAQLRLVLAIFYA 221
: | | | | | | | | | | | | | | | | | | |
Db 349 rglvflpfmvsprvcsagvlllypgwtasipillamy 386

RESULT 7
AAY29083
ID AAY29083 standard; Protein: 1199 AA.
XX AC AAY29083;
XX DT 27-SEP-1999 (first entry)
XX DE Human C1F150/hTAF1150 protein.
XX KW C1F150/hTAF1150; mitosis; cell cycle progression; neoplasia; human;
XX KW transcriptional regulator; benign proliferative disease; dysplastic;
XX KW hyperplastic disorder; anemia.
XX OS Homo sapiens.
XX PN WO9933985-A2.
XX PD 08-JUL-1999.
XX PR 28-DEC-1998; 98WO-0527665.
XX PR 30-NOV-1997; 97US-0068956.
XX PA (CHIR-) CHIRON COPP.
XX PI Kaufmann J;
XX DR WPI; 1999-444069/37.
XX DR N-PSDB; AAX91483.
XX PT New isolated IC1F150/hTAF1150 polypeptides
XX PS Claim 2; Page 78; 83pp; English.

```



```

XX Baer R, Bowcock AM;
XX WPI: 1998-230417/20;
XX N-PSDB; AAV24135;
XX
XX DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which
XX as breast cancer antigen, BRCAL, binding proteins are useful to
XX identify patient having or at risk of developing cancer
XX
XX Disclamer: Pat. 287,282, 348ff, English.
XX
XX The sequence is that of a protein which can be used in the
XX preparation of the recombinant breast cancer antigen, BRCAL, binding
XX proteins BARD1, B123, BE2, BE14, BE31 or BE445, or a composition for the
XX detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid
XX sequence, specifically a wild type BARD1 composition for the detection
XX or purification of BRCAL, useful to identify a patient having, or at
XX risk of developing cancer. BARD1 can be used in the preparation of an
XX anti-BARD1 antibody, and in the detection and purification of an
XX protein, BARD1, B123, BE2, BE14, BE31 or BE445 can be used in the
XX identification of a binding protein agonist or antagonist that alters
XX the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCAL or the
XX biological activity of the BRCAL-BARD1, B123, BE2, BE14, BE31 or BE445
XX complex. The antibodies can be used to detect BARD1, B123, BE2, BE14,
XX BE31 or BE445, a specific anti-BARD1 antibody can be used to identify
XX a patient having or at risk of developing cancer.
XX
XX Sequence 515 AA;
SQ

```

```

AAB43598
ID AAB43598 standard; Protein; 343 AA.
XX
XX AAB43598;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human cancer associated protein sequence SW2 ID B01043.
XX
XX Human; cancer associated gene, cancer antigen; detection; cancer;
XX diagnosis; metastatic; proliferative; cellular; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
XX dermatological; neuroprotective; thrombolytic; coagulant; neotropic;
XX vasodilator; antiproliferative; antineoplastic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening.
XX
XX Homo sapiens
XX
XX WC2000055350-AL.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05982.
XX
XX 12-MAR-1999; 9905-01.4270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Resen CA, Ruben SM;
XX
XX WPI: 2000-587533/55.
XX
XX N-PSDB; AA:77807.
XX
XX Novel isolated nucleic acid comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
XX Claim 17; Page 1631-1632; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
XX in AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulvovag; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
XX vasodilator; antiproliferative; antineoplastic; and angiogenic. The
XX polypeptides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the identification of
XX the present invention.
XX
XX Sequence 343 AA;
SQ

```

Query Match 0.7%; Score 71; DB 21; Length 343;
 Best Local Similarity 37.0%; Pred. No. 4.3;
 Matches 17; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1813 LATTIAPRVLLPAIKTKYKQIEKNKNHNGPMSILOEHIGXMKKE 1858

1813 LATTIAPRVLLPAIKTKYKQIEKNKNHNGPMSILOEHIGXMKKE 1858

RESULT 2

65	6.0	4.27	12	AA614346	C. ornithoglycylis-like	158	5.9	0.5	613	14	ZAR45547	CKS-HCV and lipon to
66	6.0	4.97	17	AA696326	P. citreus-like hem	159	5.9	0.5	613	22	ZAR69026	HCV recombinant an
67	6.0	5.18	20	AA696486	Buematulintin pro	160	5.9	0.5	781	13	ZAR21665	HCV CKS-48 beta - p
68	6.0	5.18	20	AA696486	Buematulintin pro	161	5.9	0.5	781	13	ZAR22208	Sequence of lipon to
69	6.0	5.41	20	AA696486	Amion acid seque	162	5.9	0.5	781	14	ZAR43634	HCV CKS-48 beta pro
70	6.0	5.41	15	AA696486	Sequence of protea	163	5.9	0.5	781	14	ZAR43634	HCV CKS-48 beta pro
71	6.0	5.41	15	AA696486	Human beta-catalase	164	5.9	0.5	781	14	ZAR43634	HCV CKS-48 beta pro
72	6.0	5.41	15	AA696486	Human beta-catalase	165	5.9	0.5	781	15	ZAR43634	HCV CKS-48 beta ant
73	6.0	5.41	15	AA696486	Human beta-catalase	166	5.9	0.5	781	15	ZAR43634	HCV recombinant an
74	6.0	5.41	15	AA696486	Human beta-catalase	167	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
75	6.0	5.41	15	AA696486	Human beta-catalase	168	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
76	6.0	5.41	15	AA696486	Human beta-catalase	169	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
77	6.0	5.41	15	AA696486	Human beta-catalase	170	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
78	6.0	5.41	15	AA696486	Human beta-catalase	171	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
79	6.0	5.41	15	AA696486	Human beta-catalase	172	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
80	6.0	5.41	15	AA696486	Human beta-catalase	173	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
81	6.0	5.41	15	AA696486	Human beta-catalase	174	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
82	6.0	5.41	15	AA696486	Human beta-catalase	175	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
83	6.0	5.41	15	AA696486	Human beta-catalase	176	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
84	6.0	5.41	15	AA696486	Human beta-catalase	177	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
85	6.0	5.41	15	AA696486	Human beta-catalase	178	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
86	6.0	5.41	15	AA696486	Human beta-catalase	179	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
87	6.0	5.41	15	AA696486	Human beta-catalase	180	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
88	6.0	5.41	15	AA696486	Human beta-catalase	181	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
89	6.0	5.41	15	AA696486	Human beta-catalase	182	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
90	6.0	5.41	15	AA696486	Human beta-catalase	183	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
91	6.0	5.41	15	AA696486	Human beta-catalase	184	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
92	6.0	5.41	15	AA696486	Human beta-catalase	185	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
93	6.0	5.41	15	AA696486	Human beta-catalase	186	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
94	6.0	5.41	15	AA696486	Human beta-catalase	187	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
95	6.0	5.41	15	AA696486	Human beta-catalase	188	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
96	6.0	5.41	15	AA696486	Human beta-catalase	189	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
97	6.0	5.41	15	AA696486	Human beta-catalase	190	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
98	6.0	5.41	15	AA696486	Human beta-catalase	191	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
99	6.0	5.41	15	AA696486	Human beta-catalase	192	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
100	6.0	5.41	15	AA696486	Human beta-catalase	193	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
101	6.0	5.41	15	AA696486	Human beta-catalase	194	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
102	6.0	5.41	15	AA696486	Human beta-catalase	195	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
103	6.0	5.41	15	AA696486	Human beta-catalase	196	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
104	6.0	5.41	15	AA696486	Human beta-catalase	197	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
105	6.0	5.41	15	AA696486	Human beta-catalase	198	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
106	6.0	5.41	15	AA696486	Human beta-catalase	199	5.9	0.5	781	15	ZAR43634	Sequence of lipon to
107	6.0	5.41	15	AA696486	Human beta-catalase	200	5.9	0.5	781	15	ZAR43634	Sequence of lipon to

ALIGNMENTS

RESULT 1

AAW54099
ID AAW54099 standard; Protein: 515 AA.

XX AC AAW54099;

XX DT 28-SEP-1998 (first entry)

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

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XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

XX DE Homo sapiens BAP28 sequence.

us-09-603-665-5.ra1

Fri Nov 9 15:42:38 2001

APPLICATION NUMBER: US 07/647,831
 FILING DATE: 29-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/FILE NUMBER: 24615 20022 00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 343 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-047-413-13

Query Match 0.6%; Score 64; DB 1; Length 343;
 Best Local Similarity 31.0%; Pred. No. 15;
 Matches 13; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1428 VLAAYGKDALEADTFEWFSSVCEFSVQHQIQSLMNIQY 1469
 :||| | | | | : : : : | | | | : | : |
 DB 167 ILANTYPPKDSIFRGEFNSFINPIIOFLVQHNPLLANVYPY 208

RESULT 6

US-08-229-050-13
 : Sequence 13, Application US/08224050
 : Patent No. 6065491
 : GENERAL INFORMATION:
 : APPLICANT: Cornelissen, Bernardus J.C.
 : APPLICANT: Melchers, Leo S.
 : APPLICANT: Meulenhoff, Elisabeth J.S.
 : APPLICANT: van Koekel, Jeroen S.C.
 : APPLICANT: Sela-Buurlage, Marianne B.
 : APPLICANT: Vloemans, Alexandra A.
 : APPLICANT: Woloshuk, Charles P.
 : APPLICANT: Bol, John F.
 : APPLICANT: Linthorst, Hubertus J.M.
 : TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
 : OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
 : POLYNUCLEOTIDES FOR USE THEREIN
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Morrison & Foerster
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/229,050
 : FILING DATE:
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/647,831
 : FILING DATE: 29-JAN-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Murashige, Kate H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/FILE NUMBER: 24615 20022 00
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-813-5600
 : TELEFAX: 415-494-0792
 : TELEX: 706141

INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 343 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-229-050-13

Query Match 0.6%; Score 64; DB 3; Length 343;
 Best Local Similarity 31.0%; Pred. No. 15;
 Matches 13; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1428 VLAAYGKDALEADTFEWFSSVCEFSVQHQIQSLMNIQY 1469
 :||| | | | | : : : : | | | | : | : |
 DB 167 ILANTYPPKDSIFRGEFNSFINPIIOFLVQHNPLLANVYPY 208

RESULT 7

US-08-801-563-13
 : Sequence 13, Application US/08801563
 : Patent No. 6087560
 : GENERAL INFORMATION:
 : APPLICANT: Cornelissen, Bernardus J.C.
 : APPLICANT: Melchers, Leo S.
 : APPLICANT: Meulenhoff, Elisabeth J.S.
 : APPLICANT: van Koekel, Jeroen S.C.
 : APPLICANT: Sela-Buurlage, Marianne B.
 : APPLICANT: Vloemans, Alexandra A.
 : APPLICANT: Woloshuk, Charles P.
 : APPLICANT: Bol, John F.
 : APPLICANT: Linthorst, Hubertus J.M.
 : TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
 : OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
 : POLYNUCLEOTIDES FOR USE THEREIN
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Morrison & Foerster
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/801,563
 : FILING DATE:
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/047,413
 : FILING DATE: 19-APR-1993
 : APPLICATION NUMBER: US 07/647,831
 : FILING DATE: 29-JAN-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Murashige, Kate H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/FILE NUMBER: 24615 20022 00
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-813-5600
 : TELEFAX: 415-494-0792
 : TELEX: 706141
 : INFORMATION FOR SEQ ID NO: 13:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 343 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-801-563-13


```

? APPLICANT: Barry, Gerard F.
? APPLICANT: Kishore, Ganesh M.
? APPLICANT: Padgett, Stephen R.
? APPLICANT: Stallings, William C.
? TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
? NUMBER OF SEQUENCES: 69
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B54F
? STREET: 700 Chesterfield Village Parkway
? CITY: St. Louis
? STATE: Missouri
? COUNTRY: USA
? ZIP: 63198
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/476,008
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/306,063
? FILING DATE: 13-SEP-1994
? TELEPHONE: (314)537-6047
? TELEFAX: (314)537-6047
? INFORMATION FOR SEQ ID NO: 63:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 426 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ATTORNEY/AGENT INFORMATION:
? NAME: Hoerner Jr., Dennis R.
? REGISTRATION NUMBER: 30,914
? REFERENCE/DOCKET NUMBER: 38-21(10660)A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (314)537-6047
? TELEFAX: (314)537-6047
? INFORMATION FOR SEQ ID NO: 63:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 426 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-476-008-63

Query Match 0.86; Score 60; DB 1; Length 426;
Best Local Similarity 47.84; Pred. No. 78;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Q7 2028 ENPLGGEEKFQFPVTKHLPICIA 2050
Db 111 EYMLGGEPMEERPIGHLVDCLA 133

RESULT 18
US-08-406-008-63
; Sequence 63, Application US/08306063
; Patent No. 5634435
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B54F
; STREET: 700 Chesterfield Village Parkway

```

```

? CITY: St. Louis
? STATE: Missouri
? COUNTRY: USA
? ZIP: 63198
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/306,063
? FILING DATE: 13-SEP-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/749,611
? FILING DATE: 28-AUG-1991
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/576,537
? FILING DATE: 31-AUG-1990
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Hoerner Jr., Dennis R.
? REGISTRATION NUMBER: 30,914
? REFERENCE/DOCKET NUMBER: 38-21(10660)A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (314)537-6047
? TELEFAX: (314)537-6047
? INFORMATION FOR SEQ ID NO: 63:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 426 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-306-063-63

Query Match 0.86; Score 60; DB 1; Length 426;
Best Local Similarity 47.84; Pred. No. 78;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Q7 2028 ENPLGGEEKFQFPVTKHLPICIA 2050
Db 111 EYMLGGEPMEERPIGHLVDCLA 133

RESULT 19
US-08-833-485-63
; Sequence 63, Application US/08833485
; Patent No. 5804425
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: 5-Ethylpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B54F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,485
; FILING DATE: 07-APR-1997

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: CLASSIFICATION: 4.6
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/744,611
: FILING DATE: 28-APR-1991
: CLASSIFICATION: 4.6
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/744,611
: FILING DATE: 28-APR-1991
: CLASSIFICATION: 4.6
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/744,611
: FILING DATE: 28-APR-1991
: CLASSIFICATION: 4.6
: NAME: Rooted, Jr., Dennis R.
: REGISTRATION NUMBER: 30,916
: REFERENCE NUMBER: 31,913
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414) 747-6099
: TELEFAX: (414) 747-6047
: INFORMATION FOR SEQ ID NO: 63:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 426 amino acids
: TYPE: amino acid
: POLYMER: linear
: MOLECULE TYPE: protein
: US-09-603-665-5
:
: Query Match: 0.68; Score 60; Id 1; Length 426;
: Best Local Similarity: 47.98; Prod. No. 78;
: Matches 11; Conservative 4; Mismatches 9; Gaps 9;
:
: 27 2028 ENPLOSPEYVPPVTRPIQCLIA 2050
: 111 EYMLGGPRMEERPGHLVLA 133
:
: RESULT 21
: 5224491-9
: Patent No. 5224491
: APPLICANT: GEN. DONALD M. D'ARD, PAUL F.
: TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
: REPLICATION
: NUMBER OF SEQUENCES: 9
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/97/482,634
: FILING DATE: 21-FEB-1990
: SEQ ID NO: 63
: LENGTH: 488
: 5224491-9
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: Query Match: 0.68; Score 60; Id 1; Length 488;
: Best Local Similarity: 57.98; Prod. No. 90;
: Matches 11; Conservative 5; Mismatches 5; Gaps 5;
:
: QY 101 LSPYFLKPAQCLFWLH 119
: 111 1111 1111 1
: Db 409 VSAVFLKPKQKCLFWLH 327
:
: RESULT 22
: US-08-570-311-2
: Sequence 2; Application US/08570411
: Patent No. 5824791
: GENERAL INFORMATION:
: APPLICANT: Proplis-Ko-Fox, Ann
: APPLICANT: Tumwasorn, Somying
: APPLICANT: Lepine, Guyline
: APPLICANT: Han, Naiming
: APPLICANT: Lantz, Marilyn
: APPLICANT: Patis, Joseph
: TITLE OF INVENTION: Cloned Porphyromonas gingivalis genes
: TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ted W. Whitlock
: STREET: 2421 N.W. 41st Street, Suite A 1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA

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: CLASSIFICATION: 4.6
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/744,611
: FILING DATE: 28-APR-1991
: CLASSIFICATION: 4.6
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/744,611
: FILING DATE: 28-APR-1991
: CLASSIFICATION: 4.6
: NAME: Rooted, Jr., Dennis R.
: REGISTRATION NUMBER: 30,916
: REFERENCE NUMBER: 31,913
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414) 747-6099
: TELEFAX: (414) 747-6047
: INFORMATION FOR SEQ ID NO: 63:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 426 amino acids
: TYPE: amino acid
: POLYMER: linear
: MOLECULE TYPE: protein
: US-09-603-665-5
:
: Query Match: 0.68; Score 60; Id 1; Length 426;
: Best Local Similarity: 47.98; Prod. No. 78;
: Matches 11; Conservative 4; Mismatches 9; Gaps 9;
:
: 27 2028 ENPLOSPEYVPPVTRPIQCLIA 2050
: 111 EYMLGGPRMEERPGHLVLA 133
:
: RESULT 21
: 5224491-9
: Patent No. 5224491
: APPLICANT: GEN. DONALD M. D'ARD, PAUL F.
: TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
: REPLICATION
: NUMBER OF SEQUENCES: 9
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/97/482,634
: FILING DATE: 21-FEB-1990
: SEQ ID NO: 63
: LENGTH: 488
: 5224491-9
:
: Query Match: 0.68; Score 60; Id 1; Length 488;
: Best Local Similarity: 57.98; Prod. No. 90;
: Matches 11; Conservative 5; Mismatches 5; Gaps 5;
:
: QY 101 LSPYFLKPAQCLFWLH 119
: 111 1111 1111 1
: Db 409 VSAVFLKPKQKCLFWLH 327
:
: RESULT 22
: US-08-570-311-2
: Sequence 2; Application US/08570411
: Patent No. 5824791
: GENERAL INFORMATION:
: APPLICANT: Proplis-Ko-Fox, Ann
: APPLICANT: Tumwasorn, Somying
: APPLICANT: Lepine, Guyline
: APPLICANT: Han, Naiming
: APPLICANT: Lantz, Marilyn
: APPLICANT: Patis, Joseph
: TITLE OF INVENTION: Cloned Porphyromonas gingivalis genes
: TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ted W. Whitlock
: STREET: 2421 N.W. 41st Street, Suite A 1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA

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? ZIP: 32606
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/570,311

? FILING DATE: 09-DEC-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/353,485
 ? FILING DATE: 09-DEC-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/647,119
 ? FILING DATE: 25-JAN-1991
 ? CLASSIFICATION: 424

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/241,640
 ? FILING DATE: 08-SEP-1988
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Whitlock, Ted W.
 ? REGISTRATION NUMBER: 36,965
 ? REFERENCE/DOCKET NUMBER: UF15.C3
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (904) 375,9169

? TELEFAX: (904) 372-5806
 ? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 497 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-570-311-2

? Query Match 0.6%; Score 60; DB 2; Length 497;
 ? Best Local Similarity 49.0%; Pred. No. 99;
 ? Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1668 QYALYTKLKCKNGAENPFFVVLXTAVKLIAP 1702
 DB 335 EAAFTKLEETIGSDKPAEMNLVRSQGVKLPAP 369

? RESULT 24
 ? US-08-453-485-2
 ? Sequence 2, Application US/08/353,485
 ? Patent No. 5830710
 ? GENERAL INFORMATION:
 ? APPLICANT: Prodisks-Prox, Ann
 ? APPLICANT: Tumwasorn, Somying
 ? APPLICANT: Lepine, Guylaine
 ? APPLICANT: Bah, Naimeq
 ? APPLICANT: Lantz, Marilyn
 ? APPLICANT: Patti, Joseph
 ? TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
 ? TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
 ? NUMBER OF SEQUENCES: 12
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Ted W. Whitlock
 ? STREET: 2421 N.W. 41st Street, Suite A-1
 ? CITY: Gainesville
 ? STATE: FL
 ? COUNTRY: USA
 ? ZIP: 32606
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US 08/353,485
 ? FILING DATE: 09-DEC-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/353,485
 ? FILING DATE: 09-DEC-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/647,119
 ? FILING DATE: 25-JAN-1991
 ? CLASSIFICATION: 424

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/241,640
 ? FILING DATE: 08-SEP-1988
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Whitlock, Ted W.
 ? REGISTRATION NUMBER: 36,965
 ? REFERENCE/DOCKET NUMBER: UF15.C3
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (904) 375,9169
 ? TELEFAX: (904) 372-5806
 ? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 497 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-353-485-2

? APPLICATION NUMBER: US/08/353,485
 ? FILING DATE: 09-DEC-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/647,119
 ? FILING DATE: 25-JAN-1991
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/241,640
 ? FILING DATE: 08-SEP-1988
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Whitlock, Ted W.
 ? REGISTRATION NUMBER: 36,965
 ? REFERENCE/DOCKET NUMBER: UF15.C2
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (904) 375,8100

? TELEFAX: (904) 372-5800
 ? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 497 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-353-485-2

? Query Match 0.6%; Score 60; DB 2; Length 497;
 ? Best Local Similarity 49.0%; Pred. No. 99;
 ? Matches 14; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1668 QYALYTKLKCKNGAENPFFVVLXTAVKLIAP 1702

DB 335 EAAFTKLEETIGSDKPAEMNLVRSQGVKLPAP 369
 ? RESULT 24
 ? US-08-460-673-2
 ? Sequence 2, Application US/08/360,673
 ? Patent No. 5679544
 ? GENERAL INFORMATION:
 ? APPLICANT: Fleet, Reinhard
 ? APPLICANT: Fournier, Alain
 ? APPLICANT: Yeh, Patrice
 ? TITLE OF INVENTION: MODIFIED KLUYVEROMYCES YEASTS, THEIR
 ? TITLE OF INVENTION: PREPARATION AND USE
 ? NUMBER OF SEQUENCES: 17
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ? STREET: 500 Arcola Rd 3043
 ? CITY: Collegeville
 ? STATE: PA
 ? COUNTRY: USA
 ? ZIP: 19002
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/360,673
 ? FILING DATE:
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/119,992, 00623
 ? FILING DATE: 23-JUN-1993
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: EP 92/07785
 ? FILING DATE: 25-JUN-1992
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Smith, Julie K.
 ? REGISTRATION NUMBER: 38,619
 ? REFERENCE/DOCKET NUMBER: STQ2040-US
 ? TELECOMMUNICATION INFORMATION:


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FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
  NAME: PERUMSKIL, PRISCILLA E
  REGISTRATION NUMBER: 44,207
  REFERENCE/IDENT NUMBER: 44,207
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 708-947-6365
  TELEFAX: 708-947-9556
  INFORMATION FOR SEQ ID NO: 47:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 594 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  US-09-603-611-47
Query Match: 58%, Score 59; 53.4; Length 594;
Best Local Similarity: 44.5%; Pred. No. 1,860,02;
Matches: 10; Conservative: 9; Mismatches: 10; Gaps: 0;
DB 4 1 VIAPAVOTNWKLETFWAKHWNFISGID 429
RESULT 35
US-09-603-611-49
Sequence 16, Application US/08867611
Patent No. 6172189
GENERAL INFORMATION:
  APPLICANT: DEVAPE, SUSHIL G
  APPLICANT: DESAI, SURESH M
  APPLICANT: CASBY, JAMES M
  APPLICANT: DAILEY, STEPHEN H
  APPLICANT: LAWSON, GEORGE J
  APPLICANT: GUTTERREZ, ROBIN A
  APPLICANT: LESNIEWSKI, RICHARD R
  APPLICANT: STEWART, JAMES L
  APPLICANT: RUPPKEHL, KEVIN P
  TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
  TITLE OF INVENTION: ANTIGEN
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
  ADDRESSER: ABBOTT LABORATORIES
  STREET: 500 ABBOTT PARK
  CITY: ABBOTT PARK
  STATE: IL
  COUNTRY: USA
  ZIP: 60064-3500
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0, Version #1.25
GENERAL APPLICATION DATA:
  APPLICATION NUMBER: US/08867611
  FILING DATE: 02-JUN-1997
  CLASSIFICATION: 4.5
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991

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FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
  NAME: PERUMSKIL, PRISCILLA E
  REGISTRATION NUMBER: 33,209
  REFERENCE/IDENT NUMBER: 44,207
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 708-947-6365
  TELEFAX: 708-947-9556
  INFORMATION FOR SEQ ID NO: 48:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 594 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  US-08-867-611-48
Query Match: 58%, Score 59; 48.4; Length 594;
Best Local Similarity: 34.5%; Pred. No. 1,860,02;
Matches: 10; Conservative: 9; Mismatches: 10; Gaps: 0;
DB 403 VIAPAVOTNWKLETFWAKHWNFISGID 441
RESULT 36
US-08-867-611-16
Sequence 16, Application US/08867611
Patent No. 6172189
GENERAL INFORMATION:
  APPLICANT: DEVAPE, SUSHIL G
  APPLICANT: DESAI, SURESH M
  APPLICANT: CASBY, JAMES M
  APPLICANT: DAILEY, STEPHEN H
  APPLICANT: LAWSON, GEORGE J
  APPLICANT: GUTTERREZ, ROBIN A
  APPLICANT: LESNIEWSKI, RICHARD R
  APPLICANT: STEWART, JAMES L
  APPLICANT: RUPPKEHL, KEVIN P
  TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
  TITLE OF INVENTION: ANTIGEN
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
  ADDRESSER: ABBOTT LABORATORIES
  STREET: 500 ABBOTT PARK
  CITY: ABBOTT PARK
  STATE: IL
  COUNTRY: USA
  ZIP: 60064-3500
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0, Version #1.25
GENERAL APPLICATION DATA:
  APPLICATION NUMBER: US/08867611
  FILING DATE: 02-JUN-1997
  CLASSIFICATION: 4.5
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/748,566
  FILING DATE: 21-AUG-1991

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? APPLICATION NUMBER: US/08/646,757
? FILING DATE:
? APPLICATION NUMBER: US/08/179,896
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/572,922
? FILING DATE: 24-AUG-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/614,069
? FILING DATE: 07 NOV 1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/748,561
? FILING DATE: 21-AUG-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/748,565
? FILING DATE: 21-AUG-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/748,566
? FILING DATE: 21-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: FOREMSKI, PRISCILLA E
? REGISTRATION NUMBER: 33,207
? REFERENCE/DOCKET NUMBER: 4834, US, IP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 708-937-6365
? TELEFAX: 708-937-9556
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 597 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-867-611-18

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Query Match 0.5%; Score 59; DB 4; Length 597;
Best Local Similarity 34.5%; Pred. No. 1.8e+02;
Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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QY 1821 VLLPAIKELVQLTKRNKSKDMSPFMSHLQ 1819
I: I::: I::: I::: I::: I::: I:::
Db 401 VIAPAVQTNWQKLETFWAKHWMNFISGIQ 429

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RESULT 37
PCT-US92 06965A-21
? Sequence 21: Application PC/US9206965A
? GENERAL INFORMATION:
? APPLICANT: DEVARE, SUSHIL G
? APPLICANT: DESAI, SURESH M
? APPLICANT: CASEY, JAMES M
? APPLICANT: DAILEY, STEPHEN H
? APPLICANT: DAWSON, GEORGE J
? APPLICANT: GUTIERREZ, ROBIN A
? APPLICANT: LESNIEWSKI, RICHARD P
? APPLICANT: STEWART, JAMES L
? APPLICANT: RUPPRECHT, KEVIN R
? TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: ABBOTT LABORATORIES
? STREET: ONE ABBOTT PARK ROAD, CHANWORTH, MA 01937
? CITY: ABBOTT PARK
? STATE: ILLINOIS
? COUNTRY: U.S.
? ZIP: 60065-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 19920821
? FILING DATE: 19920821
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: FOREMSKI, PRISCILLA E
? REGISTRATION NUMBER: 33,207
? REFERENCE/DOCKET NUMBER: 4834PC.02

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? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 708-937-6365
? TELEFAX: 708-937-9556
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 597 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PCT-US92-06965A-21

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Query Match 0.5%; Score 59; DB 5; Length 597;
Best Local Similarity 34.5%; Pred. No. 1.8e+02;
Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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QY 1821 VLLPAIKELVQLTKRNKSKDMSPFMSHLQ 1819
I: I::: I::: I::: I::: I::: I:::
Db 401 VIAPAVQTNWQKLETFWAKHWMNFISGIQ 429

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RESULT 38
US-08-867-611-18
? Sequence 18: Application US/08867611
? Patent No. 6172189
? GENERAL INFORMATION:
? APPLICANT: DEVARE, SUSHIL G
? APPLICANT: DESAI, SURESH M
? APPLICANT: CASEY, JAMES M
? APPLICANT: DAILEY, STEPHEN H
? APPLICANT: DAWSON, GEORGE J
? APPLICANT: GUTIERREZ, ROBIN A
? APPLICANT: LESNIEWSKI, RICHARD P
? APPLICANT: STEWART, JAMES L
? APPLICANT: RUPPRECHT, KEVIN R
? TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
? NUMBER OF SEQUENCES: 59
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: ABBOTT LABORATORIES
? STREET: ONE ABBOTT PARK ROAD, CHANWORTH, MA 01937
? CITY: ABBOTT PARK
? STATE: ILLINOIS
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/867,611
? FILING DATE: 02-JUN-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,757
? FILING DATE:
? APPLICATION NUMBER: US/08/179,896
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/572,822
? FILING DATE: 24-AUG-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/614,069
? FILING DATE: 07-NOV-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/748,561
? FILING DATE: 21-AUG-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/748,565
? FILING DATE: 21-AUG-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/748,566

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1  TITLE OF INVENTION: HIV SYNTHETIC PEPTIDE FROM RED MISTION
2  NUMBER OF SEQUENCES: 45
3  * CORRESPONDENCE ADDRESS:
4  ADDRESS: ABBOTT LABORATORY
5  STREET: 560 NORTH LARK PARK ROAD
6  CITY: ABBOTT PARK
7  STATE: ILLINOIS
8  COUNTRY: U.S.
9  ZIP: 60064-3500
10  * COMPUTER READABLE FORM:
11  MEDIUM TYPE: Floppy disk
12  * OPERATING SYSTEM: PC DOS/MS-DOS
13  * SOFTWARE: Patent In Release #1.0, Version #1.25
14  * CURRENT APPLICATION DATA:
15  APPLICATION NUMBER: US/08/665,444
16  FILING DATE: 1992-09-21
17  CLASSIFICATION:
18  NAME: BAILEY, DAVID Y.
19  REGISTRATION NUMBER: 443410-02
20  REFERENCE/ROCKET NUMBER: 443410-02
21  TELECOMMUNICATION INFORMATION:
22  TELEPHONE: 708-947-6065
23  TELEFAX: 708-947-6066
24  INFORMATION FOR SEQ ID NO: 1:
25  LENGTH: 84 amino acids
26  TYPE: amino acid
27  TOPOLOGY: linear
28  MOLECULE TYPE: protein
29  US/08/665,444
30  * QUERY MATCH:
31  BEST LOCAL SIMILARITY: 54.5% Score 59; ID 4; Length 85;
32  Mismatches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
33  * 1992 VIAFVQINWQKLEIIFWAKIMWNEISGID 618
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1  NAME: Bailey, David Y.
2  REGISTRATION NUMBER: 443410-02
3  REFERENCE/ROCKET NUMBER: 443410-02
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: (508) 359-4875
6  TELEFAX: (508) 359-4875
7  INFORMATION FOR SEQ ID NO: 1:
8  LENGTH: 89 amino acids
9  TYPE: amino acid
10  TOPOLOGY: linear
11  MOLECULE TYPE: protein
12  US-08-444-818-40
13  * QUERY MATCH:
14  BEST LOCAL SIMILARITY: 54.5% Score 59; ID 4; Length 85;
15  Mismatches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
16  * 1992 VIAFVQINWQKLEIIFWAKIMWNEISGID 618
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1 ADDRESS: POLY. BOND & BOND LLP
2 STREET: 400 EAST OFFICE SQUARE
3 CITY: BOSTON
4 STATE: MA
5 COUNTRY: USA
6 ZIP: 02109-2100
7 COMPUTER READABLE FORM
8 MEDIUM TYPE: FLOPPY DISK
9 OPERATING SYSTEM: IBM PC COMPATIBLE
10 SOFTWARE: PATENT IN RELEASE #1.0, Version #1.0
11 GREEN: APPLICATION DATA
12 APPLICATION NUMBER: 09/0752260
13 FILING DATE: 09/07/2000
14 CLASSIFICATION:
15 PREP APPLICATION DATA:
16 APPLICATION NUMBER: US 09/0752260
17 FILING DATE: 09/07/2000
18 TELEPHONE: 617-842-1000
19 TELEFAX: 617-842-7000
20 INFORMATION FOR SEQ ID NO: 1
21 SEQUENCE CHARACTERISTICS
22 LENGTH: 1809 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: protein
26 US 09/0752260

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Query Match
Best Local Similarity 41.4% Score 59; DB 1; Length 1809;
Matches 11; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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QY 2070 LKTPSSRPVFAALIVIALAEKENYVILP 2104

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IB 419 IVPTLQSPLESTAMUQSSVFGKKYQIFP 454

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RESULT 54
US-07-852-260-2
Sequence 2, Application US/0752260
Patent No. 5525715
GENERAL INFORMATION:
APPLICANT: Racciollo, Vincent
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 40 Rocketteller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/522,260
FILING DATE: 19920619
CLASSIFICATION: 445
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/EXCERPT NUMBER: 36607-R-P1-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0525
TELEFAX: (212) 664-0525
TELEX: 422523 COWB U1
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-852-260-2

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Query Match
Best Local Similarity 21.0% Score 11; DB 1; Length 2206;
Matches 17; Conservative 17; Mismatches 47; Indels 0; Gaps 0;

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QY 421 LKTPSSRPVFAALIVIALAEKENYVILP 2104

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IB 621 LKTPSSRPVFAALIVIALAEKENYVILP 2104

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1 REFERENCE/EXCERPT NUMBER: AIV-036-442
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: 617-842-1000
4 TELEFAX: 617-842-7000
5 INFORMATION FOR SEQ ID NO: 1
6 SEQUENCE CHARACTERISTICS:
7 LENGTH: 1809 amino acids
8 TYPE: amino acid
9 TOPOLOGY: linear
10 MOLECULE TYPE: protein
11 US 09/0752260

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Query Match
Best Local Similarity 41.4% Score 59; DB 1; Length 1809;
Matches 11; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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QY 2070 LKTPSSRPVFAALIVIALAEKENYVILP 2104

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IB 419 IVPTLQSPLESTAMUQSSVFGKKYQIFP 454

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RESULT 54
US-07-852-260-2
Sequence 2, Application US/0752260
Patent No. 5525715
GENERAL INFORMATION:
APPLICANT: Racciollo, Vincent
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 40 Rocketteller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/522,260
FILING DATE: 19920619
CLASSIFICATION: 445
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/EXCERPT NUMBER: 36607-R-P1-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0525
TELEFAX: (212) 664-0525
TELEX: 422523 COWB U1
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-852-260-2

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Query Match
Best Local Similarity 21.0% Score 11; DB 1; Length 2206;
Matches 17; Conservative 17; Mismatches 47; Indels 0; Gaps 0;

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QY 421 LKTPSSRPVFAALIVIALAEKENYVILP 2104
IB 621 LKTPSSRPVFAALIVIALAEKENYVILP 2104

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QY 541 FEIPKHFSSSEVTISNLNLF 561
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Db 681 FAMWKTYKDVQLRRKLEFF 701

RESULT 55
US-08-461-503-2
; Sequence 2, Application US/06461503
; Patent No. 5844302
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Latow, Joanne M.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
; FILING DATE: 5-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-503-2

Query Match 0.5%; Score 59; DB 2; Length 2206;
Best Local Similarity 21.0%; Prod No. 1.3e+03;
Matches 17; Conservative 17; Mismatches 47; Indels 0; Gaps 0;

QY 481 TSLMLSHLPLAVRILLAMNHLKIMKTSFGVDSFIRKAVLARLGDNDVVLISA 540
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Db 621 TAVETCATNPLASDTVQTHIVVGRPSSESTIPSPAPACACVAIVVNEQPTTRAKL 680

QY 541 FEIPKHFSSSEVTISNLNLF 561
| : : : | : : |
Db 681 FAMWKTYKDVQLRRKLEFF 701

RESULT 57
US-08-444-818-66
; Sequence 66, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Kutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESS: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: 09/094448
: FILING DATE: 14 MAR 1996
: ATTORNEY/AGENT INFORMATION
: NAME: BATHIA, ALLISA A.
: REGISTRATION NUMBER: 33,006
: REFERENCE/SECRET NUMBER: 011,002
: TELECOMMUNICATION INFORMATION
: TELEPHONE: (506) 459,8076
: TELEFAX: (506) 459,8086
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS
: LENGTH: 240 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US 09-444-818-89
:
: Query Match: 0.5% Score 59; 18.4; Length 240;
: Best Local Similarity: 34.5%; Ident. No. 1,70004;
: Matches: 11; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
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: DB 1129 VIAPAVQINWQKLETFEAKIMNMFSGIQ 1424
:
:
: RESULT 59
: PCT-US95-06722 12
: Sequence 12; Application PCT/US95/06722
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Immunosuppressant Target Proteins
: NUMBER OF SEQUENCES: 25
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (Text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/06722
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/350,795
: FILING DATE: 27 MAY 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/350,795
: FILING DATE: 20-DEC-1994
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS
: LENGTH: 2549 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-06722-12
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: Query Match: 0.5%; Score 59; 18.5; Length 2549;
: Best Local Similarity: 31.4%; Ident. No. 1,70004;
: Matches: 11; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
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: DB 1159 LVKTLQSELESTAMULSSIVFGLKKYQIFP 1194
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: RESULT 60
: US-08-444-818-89
: Sequence 25; Application US/09444818
: Patent No. 6150087
: GENERAL INFORMATION:
: APPLICANT: Chien, David Y.
: ATTORNEY/AGENT INFORMATION:
: NAME: Butler, William J.
: TITLE OF INVENTION: NANV Diagnostics and Vaccines
: NUMBER OF SEQUENCES: 777
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Charon Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: ZIP: 94608 2916
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09444818
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09444818
: FILING DATE: 14 MAR 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: BATHIA, ALLISA A.
: REGISTRATION NUMBER: 33,006
: REFERENCE/SECRET NUMBER: 011,002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (506) 459,8076
: TELEFAX: (506) 459,8086
: INFORMATION FOR SEQ ID NO: 77:
: SEQUENCE CHARACTERISTICS
: LENGTH: 240 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US 09-444-818-89
:
: Query Match: 0.5%; Score 59; 18.4; Length 240;
: Best Local Similarity: 34.5%; Ident. No. 1,70004;

```

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: APPLICATION NUMBER: 09/094448
: FILING DATE: 14 MAR 1996
: ATTORNEY/AGENT INFORMATION
: NAME: BATHIA, ALLISA A.
: REGISTRATION NUMBER: 33,006
: REFERENCE/SECRET NUMBER: 011,002
: TELECOMMUNICATION INFORMATION
: TELEPHONE: (506) 459,8076
: TELEFAX: (506) 459,8086
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS
: LENGTH: 240 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US 09-444-818-89
:
: Query Match: 0.5% Score 59; 18.4; Length 240;
: Best Local Similarity: 34.5%; Ident. No. 1,70004;
: Matches: 11; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
:
: QY 1621 VLIPATKRIYKQTEKNWKNMGPFMSILQ 1649
: 11111111111111111111111111111111
:
: DB 1295 VIAPAVQINWQKLETFEAKIMNMFSGIQ 1424
:
:
: RESULT 59
: PCT-US95-06722 12
: Sequence 12; Application PCT/US95/06722
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Immunosuppressant Target Proteins
: NUMBER OF SEQUENCES: 25
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (Text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/06722
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/350,795
: FILING DATE: 27 MAY 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/350,795
: FILING DATE: 20-DEC-1994
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS
: LENGTH: 2549 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-06722-12
:
: Query Match: 0.5%; Score 59; 18.5; Length 2549;
: Best Local Similarity: 31.4%; Ident. No. 1,70004;
: Matches: 11; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
:
: QY 2070 LKTPSSKPPFPAALIVIALAFKFFNYVILP 2104
: 11111111111111111111111111111111
:
: DB 1159 LVKTLQSELESTAMULSSIVFGLKKYQIFP 1194
:
:
: RESULT 60
: US-08-444-818-89
: Sequence 25; Application US/09444818
: Patent No. 6150087
: GENERAL INFORMATION:
: APPLICANT: Chien, David Y.
: ATTORNEY/AGENT INFORMATION:
: NAME: Butler, William J.
: TITLE OF INVENTION: NANV Diagnostics and Vaccines
: NUMBER OF SEQUENCES: 777
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Charon Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: ZIP: 94608 2916
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09444818
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09444818
: FILING DATE: 14 MAR 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: BATHIA, ALLISA A.
: REGISTRATION NUMBER: 33,006
: REFERENCE/SECRET NUMBER: 011,002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (506) 459,8076
: TELEFAX: (506) 459,8086
: INFORMATION FOR SEQ ID NO: 77:
: SEQUENCE CHARACTERISTICS
: LENGTH: 240 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US 09-444-818-89
:
: Query Match: 0.5%; Score 59; 18.4; Length 240;
: Best Local Similarity: 34.5%; Ident. No. 1,70004;

```



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Query Match: 0.58; Score: 59; Len: 4; Length: 2894;
Best Local Similarity: 34.58; Pred. No.: 20004;
Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

QY 1821 VLIPALFKYVGFNFNMHMFNSHQ 1649
   1 111 1111 1 11 11 11
DB 1745 VIAVAVQVNWKELEFWAKBMRNFSGIQ 1773

RESULT 64
US-09-275-265-23
Sequence 23, Application US/09275265
Patent No. 6,297,761
GENERAL INFORMATION:
APPLICANT: DELAYS, ROBERT J
APPLICANT: POLLET, DIRK
APPLICANT: MAITIENS, GEERT
APPLICANT: VAN HEUVERSWIN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: RIXER & VAN DERHUYE P.O.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/86/091,671
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: 55,377,420,286
FILING DATE: 14-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 91/0791/02409
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90134241.2
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SADDIFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/BOOKLET NUMBER: 1387-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-275-265-23

Query Match: 0.58; Score: 59; Len: 4; Length: 2894;
Best Local Similarity: 34.58; Pred. No.: 20004;
Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

QY 1821 VLIPALFKYVGFNFNMHMFNSHQ 1649
   1 111 1111 1 11 11 11
DB 1745 VIAVAVQVNWKELEFWAKBMRNFSGIQ 1773

RESULT 64
US-09-275-265-23
Sequence 23, Application US/09275265
Patent No. 6,297,761
GENERAL INFORMATION:
APPLICANT: DELAYS, ROBERT J
APPLICANT: POLLET, DIRK
APPLICANT: MAITIENS, GEERT
APPLICANT: VAN HEUVERSWIN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: RIXER & VAN DERHUYE P.O.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/86/091,671
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: 55,377,420,286
FILING DATE: 14-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 91/0791/02409
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90134241.2
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SADDIFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/BOOKLET NUMBER: 1387-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-275-265-23

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INFORMATION: "There is a heterogeneity at


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OTHER INFORMATION: Xaa which is either Gly or Val"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2349
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Thr or Ser"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2385
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Tyr or Phe"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2386
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Ser or Ala"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2502
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Leu or Phe"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2690
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Arg or Gly"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2921
OTHER INFORMATION: /note= "A heterogeneity exists at
OTHER INFORMATION: Xaa which is either Arg or Gly"
US-08-444-818-124

Query Match 0.5%; Score 59; DB 4; Length 2955;
Best Local Similarity 34.5%; Pred. R6; 2.1e+03;
Matches 16; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1821 VLLPALKFTYKQIEKKNKNNMPPFMSILQ 1849
1: 111: 1111 1 1 1 11 11 11
Db 1745 VVAFVQTRWQLETWAKMWHFISIQ 1773

RESULT 69
US-08-249-843-3
Sequence 3, Application US/08249843
Patent No. 6274148
GENERAL INFORMATION:
APPLICANT: RALSTON, ROBERT O.
APPLICANT: MARCUS, FRANK
APPLICANT: THUDUM, KENT B.
APPLICANT: GERVAISE, BARBARA A.
APPLICANT: HALL, JOHN A.
TITLE OF INVENTION: HEPATITIS C VIRUS ANTIALCOLOPROTEINS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249.843
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HARBIN, ALISA A.

```

```

REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0154 003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2955 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Arg or Lys"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Asn or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 176
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Ile or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 334
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Met or Val"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 603
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Ile or Leu"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 848
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Asn or Tyr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1114
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Pro or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1117
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Ser or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1276
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Leu or Pro"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1454
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Cys or Tyr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1471
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Ser or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1877
OTHER INFORMATION: /note= "There is a heterogeneity at
OTHER INFORMATION: this location; Xaa = Glu or Gly"
FEATURE:

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NAME/KEY: Modified site
 LOCATION: 1049
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa His or Lys"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 1049
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Cys or Ser"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2121
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Gly or Val"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2449
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Ser or Thr"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2509
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Ala or Ser"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2509
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Ile or Leu"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2921
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Gly or Ala"
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 2921
 OTHER INFORMATION: Note "There is a heterogeneity at this location: Xaa Ala or Gly"
 US-09-603-665-5

Query Match 0.58; Score 59; DB 4; Length 2955;
 Best Local Similarity 4.58; Prod. No. 211004;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLPAIKKRYGTEKNWNNHPEMSILQ 1849
 EL 1745 VLPAVLTNWKLEIKWKBNNHPEMSILQ 1774

RESULT 71
 US-09-603-665-5
 Sequence 2, Application US/0844552
 Patent No. 5667992

GENERAL INFORMATION:
 APPLICANT: CHIBO, DAVID Y.
 APPLICANT: PARTNER, WILLIAM J.
 TITLE OF INVENTION: NARROW GLAUCOMAS AND VASCULOS
 NUMBER OF SEQUENCES: 99
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chibon Corporation
 STREET: 1500 Barton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608-2016
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/009,444,818
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,590
 FILING DATE: 14-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbin, Alison A.
 REGISTRATION NUMBER: 33,895
 REFERENCE/EXCIT NUMBER: 6113,902
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 359-4885
 TELEFAX: (508) 359-4885
 INFORMATION FOR SEQ ID NO: 148:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2955 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-444-818-148

Query Match 0.58; Score 59; DB 4; Length 2955;
 Best Local Similarity 4.58; Prod. No. 211004;
 Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLPAIKKRYGTEKNWNNHPEMSILQ 1849
 EL 1745 VLPAVLTNWKLEIKWKBNNHPEMSILQ 1774

RESULT 71
 US-08-453-552-2
 Sequence 2, Application US/0845352
 Patent No. 5667992

GENERAL INFORMATION:
 APPLICANT: CASEY, JAMES M.
 APPLICANT: BOBE, SUZANNE L.
 APPLICANT: ZETK, BILLY J.
 APPLICANT: YAMAGUCHI, JULIE
 APPLICANT: FRAIL, DONALD E.
 APPLICANT: DESAI, SURESH M.
 APPLICANT: DEVARE, SUSHIL G.
 TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: ONE ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/009,453,552
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,247
 REFERENCE/EXCIT NUMBER: 6141,US,11
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365

DB 1745 VIAPAVQTNWQKLETFWAKHMMNFISGIQ 1773

RESULT 73

US-08-440-542-36

Sequence 36, Application US/08440542

Patent No. 5670153

GENERAL INFORMATION:

APPLICANT: Weiner, Amy J.

APPLICANT: Houghton, Michael

TITLE OF INVENTION: Immunoreactive Polypeptide Compositions

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-440-542

FILING DATE: 12-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/231,368

FILING DATE:

APPLICATION NUMBER: US 07/759,575

FILING DATE: 13-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: McClung, Barbara G.

REGISTRATION NUMBER: 33,113

REFERENCE/DECKET NUMBER: 0205,001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2708

TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 3011 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-440-542-36

Query Match 0.5%; Score 59; DB 1; Length 3011;

Best Local Similarity 34.5%; Pred. No. 2.2e+03;

Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPAITFTTQIEFKNNKHMGPMSIIQ 1849

1: 111: 111: 11 11 11 11

DB 1745 VIAPAVQTNWQKLETFWAKHMMNFISGIQ 1773

RESULT 74

US-07-910-760-10

Sequence 10, Application US/07910760

Patent No. 5683864

GENERAL INFORMATION:

APPLICANT: Houghton, Michael

APPLICANT: Choo, Qui-lim

TITLE OF INVENTION: Combinations of Hepatitis B virus (HBV)

TITLE OF INVENTION: Antigens for use in immunoassays for Anti-HCV Antibodies

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: P O Box 8047 (Int. Prop. R-440)

QY 1821 VLLPAITFTTQIEFKNNKHMGPMSIIQ 1849

1: 111: 111: 11 11 11 11

DB 1745 VIAPAVQTNWQKLETFWAKHMMNFISGIQ 1773

RESULT 72

US-08-440-104-36

Sequence 36, Application US/08440105

Patent No. 5670152

GENERAL INFORMATION:

APPLICANT: Weiner, Amy J.

APPLICANT: Houghton, Michael

TITLE OF INVENTION: Immunoreactive Polypeptide Compositions

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,103

FILING DATE: 12-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/231,368

FILING DATE:

APPLICATION NUMBER: US 07/759,575

FILING DATE: 13-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: McClung, Barbara G.

REGISTRATION NUMBER: 33,113

REFERENCE/DECKET NUMBER: 0205,001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2708

TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 3011 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-440-104-36

Query Match 0.5%; Score 59; DB 1; Length 3011;

Best Local Similarity 34.5%; Pred. No. 2.2e+03;

Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1821 VLLPAITFTTQIEFKNNKHMGPMSIIQ 1849

1: 111: 111: 11 11 11 11

CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94602-6009
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BOOTHBY, ESTHER BOOTHBY
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94608

Query Match: 0.58; Score 59; DB 1; Length 4011
 Best Local Similarity: 34.58; Freq. No. 2,260,043
 Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

09 1821 VILFAIKRIKVEJLEKRWENIMGFPSHIG 1849
 10 1745 VIAFAVQTNWQKLETFWAKHWNFISGIG 1774

RESULT 76
 US-08-241-368-46
 Sequence 36, Application US/08231468
 Patent No. 5756412
 GENERAL INFORMATION:
 APPLICANT: Weibull, Amy J.
 APPLICANT: Boothby, Michael
 TITLE OF INVENTION: Immunoreactive polypeptide compositions
 NUMBER OF SEQUENCES: 45
 REFERENCE ADDRESS:
 ADDRESS: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Boothby, Michael
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94602-6009
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BOOTHBY, ESTHER BOOTHBY
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94608

Query Match: 0.58; Score 59; DB 1; Length 4011
 Best Local Similarity: 34.58; Freq. No. 2,260,043
 Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

09 1821 VILFAIKRIKVEJLEKRWENIMGFPSHIG 1849
 10 1745 VIAFAVQTNWQKLETFWAKHWNFISGIG 1774

CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94602-6009
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BOOTHBY, ESTHER BOOTHBY
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94608

Query Match: 0.58; Score 59; DB 1; Length 4011
 Best Local Similarity: 34.58; Freq. No. 2,260,043
 Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

09 1821 VILFAIKRIKVEJLEKRWENIMGFPSHIG 1849
 10 1745 VIAFAVQTNWQKLETFWAKHWNFISGIG 1774

RESULT 76
 US-08-241-368-46
 Sequence 36, Application US/08231468
 Patent No. 5756412
 GENERAL INFORMATION:
 APPLICANT: Weibull, Amy J.
 APPLICANT: Boothby, Michael
 TITLE OF INVENTION: Immunoreactive polypeptide compositions
 NUMBER OF SEQUENCES: 45
 REFERENCE ADDRESS:
 ADDRESS: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Boothby, Michael
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94602-6009
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 MEDIUM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Process #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/77410, 760
 FILING DATE: 07/01/1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Boothby, Michael
 REFERENCE NUMBER: 435
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 601-2702
 INFORMATION REFERENCE ADDRESS:
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94608

Query Match: 0.58; Score 59; DB 1; Length 4011
 Best Local Similarity: 34.58; Freq. No. 2,260,043
 Matches: 10; Conservative: 9; Mismatches: 10; Indels: 0; Gaps: 0;

09 1821 VILFAIKRIKVEJLEKRWENIMGFPSHIG 1849
 10 1745 VIAFAVQTNWQKLETFWAKHWNFISGIG 1774

APPLICANT: Chiron, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NABV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/008,444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,403,500
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbio, Alisa A.
REGISTRATION NUMBER: 43,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 359-3876
TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Duplication
LOCATION: 9
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Lys or Arg"
FEATURE:
NAME/KEY: Duplication
LOCATION: 11
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Asn or Thr"
FEATURE:
NAME/KEY: Duplication
LOCATION: 176
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Ile or Thr"
FEATURE:
NAME/KEY: Duplication
LOCATION: 334
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Met or Val"
FEATURE:
NAME/KEY: Duplication
LOCATION: 603
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Leu or Ile"
FEATURE:
NAME/KEY: Duplication
LOCATION: 848
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Tyr or Asn"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1114
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Pro or Ser"
FEATURE:

NAME/KEY: Duplication
LOCATION: 1117
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Ser or Thr"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1276
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Pro or Leu"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1454
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Cys or Tyr"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1471
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Thr or Ser"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1877
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Glu or Gly"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1948
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Leu or His"
FEATURE:
NAME/KEY: Duplication
LOCATION: 1949
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Ser or Cys"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2021
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Gly or Val"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2349
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Thr or Ser"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2385
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Tyr or Phe"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2386
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Ser or Ala"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2502
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa = Leu or Phe"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2690
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Arg or Gly"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2921
OTHER INFORMATION: /note= "There exists a
OTHER INFORMATION: heterogeneity at this position - Xaa - Arg or Gly"
FEATURE:
NAME/KEY: Duplication
LOCATION: 2996
OTHER INFORMATION: /note= "There exists a

PCT-US93-00907-2

? Sequence 2, Application PC/TUS9300907

? GENERAL INFORMATION:

? APPLICANT: CASEY, JAMES M.

? APPLICANT: BODE, SUZANNE L.

? APPLICANT: ZECK, BILLY J.

? APPLICANT: YAMAGUCHI, JULIE

? APPLICANT: FRAIL, DONALD E.

? APPLICANT: DESAI, SURESH M.

? APPLICANT: DEVAKE, SURESH G.

? TITLE OF INVENTION: MAMMALIAN EXPRESSION CYCLES FOR HCV

? TITLE OF INVENTION: PROTEINS

? NUMBER OF SEQUENCES: 12

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: ABBOTT LABORATORIES 3477 AVE D

? STREET: ONE ABBOTT PARK ROAD

? CITY: ABBOTT PARK

? STATE: IL

? COUNTRY: USA

? ZIP: 60964-1500

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent in Release #1.0, Version #1.25

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: PCT/US93/00907

? FILING DATE: 19930129

? CLASSIFICATION:

? ATTORNEY/AGENT INFORMATION:

? NAME: JORMASKI, PRISCILLA E.

? REGISTRATION NUMBER: 33,207

? REFERENCE/DOCKET NUMBER: 5131.PC.01

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: 708-937-6365

? TELEFAX: 708-937-9556

? INFORMATION FOR SEQ ID NO: 2:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 3011 amino acids

? TYPE: AMINO ACID

? STRANDEDNESS: single

? TOPOLOGY: linear

? MOLECULE TYPE: protein

? PCT-US93-00907-2

Query Match 6.5%, Score 59; DB 5; Length 3611;

Best Local Similarity 34.5%; Pred. No. 2,26+03;

Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 182 YLLSAAGKRVVETLEHISVYFETGILISQVLEKITSSESSASQAHRIETLKKTLAT 1815

DB 174 VIALAVQTNWGLETFWAKHWNFTSGIQ 1773

RESULT 86

US-08-209-1820-4

? Sequence 4, Application US/082091820

? Patent No. 5545537

? GENERAL INFORMATION:

? APPLICANT: Skelly, Susan M.

? APPLICANT: Tackney, Charles T.

? APPLICANT: Snowwaert, John R.

? APPLICANT: Fowlkes, Dana M.

? TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins

? NUMBER OF SEQUENCES: 22

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Imclone Systems Incorporated

? STREET: 180 Varick Street

? CITY: New York

? STATE: New York

? COUNTRY: United States

? ZIP: 10014

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent in Release #1.0, Version #1.25

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: 95/08/299,182C

? FILING DATE: 10-MAR-1994

? PRIOR APPLICATION DATA:

? APPLICATION NUMBER: US 07/724,698

? FILING DATE: 02-10-1991

? ATTORNEY/AGENT INFORMATION:

? NAME: Peit, Irving N.

? REGISTRATION NUMBER: 28,601

? REFERENCE/DOCKET NUMBER: SKE-1-PD

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: 212-645-1405

? TELEFAX: 212-645-2054

? INFORMATION FOR SEQ ID NO: 4:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 181 amino acids

? TYPE: amino acid

? TOPOLOGY: linear

? MOLECULE TYPE: protein

? US-08-209-1820-4

Query Match 0.5%; Score 58; DB 1; Length 181;

Best Local Similarity 22.5%; Pred. No. 40;

Matches 18; Conservative 16; Mismatches 46; Indels 0; Gaps 0;

QY 1756 YLLSAAGKRVVETLEHISVYFETGILISQVLEKITSSESSASQAHRIETLKKTLAT 1815

DB 28 YLLGISALEFEISNFCMMSESSFAAFAPRNILPMARFQANFCSSFNFTTSVYLLIG 87

QY 1816 TLAPVLLPAIKTKYQIEK 1835

DB 88 LLEPEVYLEYIQNRFESSEE 107

RESULT 87

PCT-US92-05612-4

? Sequence 4, Application PC/TUS9205612

? GENERAL INFORMATION:

? APPLICANT: Skelly, Susan M.

? APPLICANT: Tackney, Charles T.

? APPLICANT: Snowwaert, John N.

? APPLICANT: Fowlkes, Dana M.

? TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins

? NUMBER OF SEQUENCES: 8

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Imclone Systems Incorporated

? STREET: 180 Varick Street

? CITY: New York

? STATE: New York

? COUNTRY: United States

? ZIP: 10014

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent in Release #1.0, Version #1.25

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: PCT/US92/05612

? FILING DATE: 19920702

? CLASSIFICATION: 530

? ATTORNEY/AGENT INFORMATION:

? NAME: Peit, Irving N.

? REGISTRATION NUMBER: 28,601

? REFERENCE/DOCKET NUMBER: SKE-1-PT

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: 212-645-1405

? TELEFAX: 212-645-2054

? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/357,642A
 ? FILING DATE: December 15, 1994
 ? CLASSIFICATION: 536
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Warburg, Richard J.
 ? REGISTRATION NUMBER: 32,327
 ? REFERENCE/DOCKET NUMBER: 32,327
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? LENGTH: 1009
 ? SEQUENCE CHARACTERISTICS:
 ? INFORMATION FOR SEQ ID NO: 1:
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? US-08-357-642A-1

Query Match 0.58; Score 58; DB 2; Length 1009;
 Best Local Similarity 23.38; Pred. No. 5,6e+02;
 Matches 10; Conservative 13; Mismatches 20; Indels 0; Gaps 0;
 QY 1203 YWQEVTLLELLQHKRLKPSQIIIVPTIFNLSQCTFPDQEQ 1245
 DB 627 FLELNKIVICVLEKGDPLKPDLCPPVITIMFCWYDPSDR 669

RESULT 96
 US-08-460-626-1
 ? Sequence 1; Application US/08410526
 ? Patent No. 5937815
 ? GENERAL INFORMATION:
 ? APPLICANT: SIMA LEV
 ? TITLE OF INVENTION: PVA 2 RELATED PROJECTS ARE
 ? TITLE OF INVENTION: METHODS
 ? NUMBER OF SEQUENCES: 25
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Lyon & Lyon
 ? STREET: 633 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071-2066
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/460,626
 ? FILING DATE: June 2, 1995
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/357,642
 ? FILING DATE: December 15, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Warburg, Richard J.
 ? REGISTRATION NUMBER: 32,327
 ? REFERENCE/DOCKET NUMBER: 32,327
 ? TELECOMMUNICATION INFORMATION:

? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? LENGTH: 1009
 ? SEQUENCE CHARACTERISTICS:
 ? INFORMATION FOR SEQ ID NO: 1:
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? US-08-460-626-1

Query Match 0.58; Score 58; DB 2; Length 1009;
 Best Local Similarity 23.38; Pred. No. 5,6e+02;
 Matches 10; Conservative 13; Mismatches 20; Indels 0; Gaps 0;
 QY 1203 YWQEVTLLELLQHKRLKPSQIIIVPTIFNLSQCTFPDQEQ 1245
 DB 627 FLELNKIVICVLEKGDPLKPDLCPPVITIMFCWYDPSDR 669

RESULT 97
 US-08-477-451-11
 ? Sequence 11; Application US/08477451
 ? Patent No. 5928865
 ? GENERAL INFORMATION:
 ? APPLICANT: Covacci, Antonello
 ? TITLE OF INVENTION: Bacteriophage T4-like Region
 ? NUMBER OF SEQUENCES: 46
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Chiron Corporation
 ? STREET: 4560 Horton Street
 ? CITY: Emeryville
 ? STATE: CA
 ? COUNTRY: USA
 ? ZIP: 94608-2916
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? OPERATING SYSTEM: IBM PC compatible
 ? SOFTWARE: Patent in Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/477,451
 ? FILING DATE: 07-MAR-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: McClung, Barbara G.
 ? REGISTRATION NUMBER: 33,113
 ? REFERENCE/DOCKET NUMBER: 0335,002
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 510-601-2708
 ? TELEFAX: 510-655-3542
 ? INFORMATION FOR SEQ ID NO: 11:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1781 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-477-451-11

Query Match 0.58; Score 58; DB 2; Length 1781;
 Best Local Similarity 38.58; Pred. No. 1.3e+03;
 Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 1633 WKFTIVTFLKIVPTIATVQPKKKE 1658
 DB 547 WSKKITTKILQASLAIITQKKMKO 572

RESULT 98

TELECOMMUNICATION INFORMATION:

us-09-603-665-5.ra1

Fri Nov 9 15:42:38 2001

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-654-2

Query Match 0.5%; Score 57; DB 1; Length 351;
Best Local Similarity 22.4%; Pred. No. 1.5e+02;
Matches 13; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

67 1479 ETIKAVSNKSKSQHMLGVNVEHTSQI PRFPLSVSPMSQLSSNNPLKKVVE 1536
1 3 : : 1 1 1 : : : : : 1 : 1 1 1 : : : 1 1 1 : : 1 1 1 : :
Db 175 EDVQHILATSSNQRYVRMLDLQIKSAKETIKETIVTSFQPTTQNLQPLQPE 232

RESULT 112
US-08-995-654-2
Sequence 2, Application US/08995654
Patent No. 6025138
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig
APPLICANT: Sellhammer, Jeffrey
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 4174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08995654
FILING DATE: December 22, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,178
FILING DATE: August 20, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0028-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-995-654-2

Query Match 0.5%; Score 57; DB 1; Length 351;
Best Local Similarity 22.4%; Pred. No. 1.5e+02;
Matches 13; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 1479 ETIPAVSNKSKSQHMLGVNVEHTSQI PRFPLSVSPMSQLSSNNPLKKVVE 1536

1 3 : : 1 1 1 : : : : : 1 : 1 1 1 : : : 1 1 1 : : 1 1 1 : :
Db 175 EDVQHILATSSNQRYVRMLDLQIKSAKETIKETIVTSFQPTTQNLQPLQPE 232

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-654-2

Query Match 0.5%; Score 57; DB 1; Length 351;
Best Local Similarity 22.4%; Pred. No. 1.5e+02;
Matches 13; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

67 1479 ETIKAVSNKSKSQHMLGVNVEHTSQI PRFPLSVSPMSQLSSNNPLKKVVE 1536
1 3 : : 1 1 1 : : : : : 1 : 1 1 1 : : : 1 1 1 : : 1 1 1 : :
Db 175 EDVQHILATSSNQRYVRMLDLQIKSAKETIKETIVTSFQPTTQNLQPLQPE 232

RESULT 113
US-08-415-823-2
Sequence 2, Application US/08415823
Patent No. 5759538
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yaping
TITLE OF INVENTION: BACILLUS THURINGIENSIS apt AND DPT
TITLE OF INVENTION: PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
TITLE OF INVENTION: PROTEASE DEFICIENT B.T. STRAINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fanitch Schwabe Jacobs & Nadel, P.C.
STREET: 1601 Market Street, 36th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08415823
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-823-2

Query Match 0.5%; Score 57; DB 1; Length 397;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1720 LTNITMSIFTFMCAVNPMLDITVYSPOVI 1346
1 3 : : 1 1 1 : : : : : 1 : 1 1 1 : : : 1 1 1 : : 1 1 1 : :
Db 50 LSNVQSPHKSVGANVLSKDKDKLGFVW 76

RESULT 114
US-09-086-662-2
Sequence 2, Application US/09086662
Patent No. 5962264
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yaping
TITLE OF INVENTION: BACILLUS THURINGIENSIS apt AND DPT
TITLE OF INVENTION: PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
TITLE OF INVENTION: PROTEASE DEFICIENT B.T. STRAINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fanitch Schwabe Jacobs & Nadel, P.C.
STREET: 1601 Market Street, 36th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible


```

? Patent No. 5976545
? GENERAL INFORMATION:
? APPLICANT: Harris Ph.D., Jeffrey D.
? APPLICANT: Hsu, Kuang T.
? APPLICANT: Podolski, Joseph S.
? TITLE OF INVENTION: Pharmaceutical Compositions for
? TITLE OF INVENTION: Immunocontraception
? NUMBER OF SEQUENCES: 61
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
? ADDRESS: Borun
? STREET: 6300 Sears Tower, 233 South Wacker Drive
? CITY: Chicago
? STATE: Illinois
? COUNTRY: United States of America
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,158B
? FILING DATE: 07-JUNE-95
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09-NOV-92
? FILING DATE: 09-NOV-92
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/012,990
? FILING DATE: 29-JAN-93
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/973,341
? FILING DATE: 09-NOV-92
? ATTORNEY/AGENT INFORMATION:
? NAME: Clough, David W.
? REGISTRATION NUMBER: 36,107
? REFERENCE/DOCKET NUMBER: 32744
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6653
? TELEFAX: 312/474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-484-158B-16

Query Match 0.5% Score 57; DB 2; Length 570;
Best Local Similarity 27.3%; Pred No. 3,26+02;
Matches 12; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Q7 702 VTFHVILSVLVCSSSIKTHPEPAIVFSLIQKIKKLESVIT 745
:| | | | | | | | | | | | | | | | | | | | |
Db 408 ITRUSIFELRVSCSYSVKSNAPFISVQVFTIPPHUKTGHGPLE 351

RESULT 119
US-08-484-158B-16
; Sequence 16, Application US/08484158B
; Patent No. 5981228
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223

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```

? CITY: Chicago
? STATE: Illinois
? COUNTRY: United States of America
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,596A
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/149,223
? FILING DATE: 11-NOV-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/973,341
? FILING DATE: 09-NOV-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Clough, David W.
? REGISTRATION NUMBER: 36,107
? REFERENCE/DOCKET NUMBER: 31745
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/474-6653
? TELEFAX: 312/474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-484-596A-16

Query Match 0.5% Score 57; DB 2; Length 570;
Best Local Similarity 27.3%; Pred No. 3,26+02;
Matches 12; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Q7 702 VTFHVILSVLVCSSSIKTHPEPAIVFSLIQKIKKLESVIT 745
:| | | | | | | | | | | | | | | | | | | | |
Db 308 ITRUSIFELRVSCSYSVKSNAPFISVQVFTIPPHUKTGHGPLE 351

RESULT 119
US-08-480-150A-16
; Sequence 16, Application US/08480150A
; Patent No. 5989550
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223

```



```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-046-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-451-747-21

Query Match 0.5%; Score 57; DB 2; Length 591;
Best Local Similarity 29.9%; Pred. No. 3 4 0 0 0;
Matches 14; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 1348 KTKVMVIPALIQSDGDSIEVSRNVEIIVKLIISVFDALPHVPEHR 1394
Db 208 KTKMKKKKKPFSEVDFQIFCTGVVPEARQLSSVKAEDLPDEPDHQ 254

RESULT 124
US-09-134-852-21
; Sequence 21, Application US/09134852
; Patent No. 6127148
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,852
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 4406
; TELECOMMUNICATION INFORMATION:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,995A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 4406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-145-995A-21

Query Match 0.5%; Score 57; DB 1; Length 591;
Best Local Similarity 29.8%; Pred. No. 3 4 0 0 2;
Matches 14; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 1348 KTKVMVIPALIQSDGDSIEVSRNVEIIVKLIISVFDALPHVPEHR 1394
Db 208 KTKMKKKKKPFSEVDFQIFCTGVVPEARQLSSVKAEDLPDEPDHQ 254

RESULT 123
US-08-451-747-21
; Sequence 21, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLOGICS, INC.
; STREET: 32 TOWER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:

```



```

US-08-961-810-123
: Sequence 123, Application US/08961810
: Patent No. 6165713
: GENERAL INFORMATION:
: APPLICANT: Liskay, Robert M.
: APPLICANT: Brenner, C. Eric
: APPLICANT: Baker, Sean M.
: APPLICANT: Bellay, Roni J.
: APPLICANT: Kolodner, Richard D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
: TITLE OF INVENTION: MISMATCH REPAIR GENES
: NUMBER OF SEQUENCES: 134
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack &
: ADDRESSEE: Heuser
: STREET: 520 S.W. Yamhill Street, Suite 200
: CITY: Portland
: STATE: Oregon
: COUNTRY: U.S.A.
: ZIP: 97204
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,810
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Van Rysselberghe, Pierre C.
: REGISTRATION NUMBER: 33,557
: REFERENCE/DOCKET NUMBER: OHSU 3066
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (503) 224-6655
: TELEFAX: (503) 295-6679
: TELEX: 360619
: INFORMATION FOR SEQ ID NO: 123:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 770 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: QUERY MATCH 0.5% Score 57; DB 4; Length 770;
: Best Local Similarity 32.4% Pred No 5,1e-02;
: Matches 12; Conservative 7; Mismatches 18; Indels 0; Caps 0;
:
: Q7 1479 ETIPKAVSPKSKSECPMQLQVFNVTHTSKQLRHKF 1515
:
: Db 701 DMVPKVDLDAISEDEKAQFINRKEHSSLSLEHVL 737
:
: RESULT 129
: US-08-452-9620-123
: Sequence 124, Application US/084529620
: Patent No. 6191268
: GENERAL INFORMATION:
: APPLICANT: Liskay, Robert M.
: APPLICANT: Brenner, C. Eric
: APPLICANT: Baker, Sean M.
: APPLICANT: Bellay, Roni J.
: APPLICANT: Kolodner, Richard D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
: TITLE OF INVENTION: MISMATCH REPAIR GENES
: NUMBER OF SEQUENCES: 149
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack &
: ADDRESSEE: Heuser
: STREET: 520 S.W. Yamhill Street, Suite 200

```

```

: CITY: Portland
: STATE: Oregon
: COUNTRY: U.S.A.
: ZIP: 97204
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/352-9020
: FILING DATE: 09-Dec-1994
: CLASSIFICATION: unknown
: ATTORNEY/AGENT INFORMATION:
: NAME: Van Rysselberghe, Pierre C.
: REGISTRATION NUMBER: 33,557
: REFERENCE/DOCKET NUMBER: OHSU 3066
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (503) 224-6655
: TELEFAX: (503) 295-6679
: TELEX: 360619
: INFORMATION FOR SEQ ID NO: 123:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 770 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: QUERY MATCH 0.5% Score 57; DB 4; Length 770;
: Best Local Similarity 32.4% Pred No 5,1e-02;
: Matches 12; Conservative 7; Mismatches 18; Indels 0; Caps 0;
:
: Q7 1479 ETIPKAVSPKSKSECPMQLQVFNVTHTSKQLRHKF 1515
:
: Db 701 DMVPKVDLDAISEDEKAQFINRKEHSSLSLEHVL 737
:
: RESULT 130
: US-09-070-060-3
: Sequence 3, Application US/09070060
: Patent No. 5976849
: GENERAL INFORMATION:
: APPLICANT: Hustad, Carolyn M.
: APPLICANT: Chidyal, Namit
: TITLE OF INVENTION: Human E3 Ubiquitin Protein
: TITLE OF INVENTION: Ligase
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ZENECA Pharmaceuticals, Inc.
: STREET: 1800 Concord Pike
: CITY: Wilmington
: STATE: DE
: COUNTRY: USA
: ZIP: 19850-5437
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/070,060
: FILING DATE: 30-APR-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/073,839
: FILING DATE: 05-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Higgins, Patrick II
: REGISTRATION NUMBER: 39,709

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? CLASSIFICATION: 445
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/170558
? FILING DATE: 20-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/157563
? FILING DATE: 23-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 854C12
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/425-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 888 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-445-640-35

Query Match 0.5%; Score 57; DB 1; Length 888;
Best Local Similarity 23.3%; Pred. No. 6.4e+02;
Matches 14; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1210 ILELQHKKLESPVLTPIPNLSPTLPPQPGNMMETKGLISGLINICOKLSPD 1269
DB 752 IYDILQGNLKPQVDFLDGLIXLSMSRWELNDRDPSFAELREDLENTLKALPPAQEPD 811

```

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RESULT 144
US-08-170-558-35
? Sequence 35, Application US/08170558
? Patent No. 6001621
? GENERAL INFORMATION:
? APPLICANT: Godowski, Paul J.
? APPLICANT: Mark, Melanie R.
? APPLICANT: Scadden, David T.
? APPLICANT: Baker, Kevin P.
? APPLICANT: Baron, Will F.
? TITLE OF INVENTION: Protein Tyrosine Kinases
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 08-04-170-558
? FILING DATE: 20-DEC-1993
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/157563
? FILING DATE: 23-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 854C11
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/425-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 888 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-445-640-35

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```

? LENGTH: 888 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-170-558-35

Query Match 0.5%; Score 57; DB 1; Length 888;
Best Local Similarity 23.3%; Pred. No. 6.4e+02;
Matches 14; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1210 ILELQHKKLESPVLTPIPNLSPTLPPQPGNMMETKGLISGLINICOKLSPD 1269
DB 752 IYDILQGNLKPQVDFLDGLIXLSMSRWELNDRDPSFAELREDLENTLKALPPAQEPD 811

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RESULT 135
US-08-447-314-35
? Sequence 35, Application US/08447314
? Patent No. 6087144
? GENERAL INFORMATION:
? APPLICANT: Scadden, David T.
? APPLICANT: Baker, Kevin P.
? APPLICANT: Baron, Will F.
? TITLE OF INVENTION: Protein Tyrosine Kinases
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patin (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/447,314
? FILING DATE: 22-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/170558
? FILING DATE: 20-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/157563
? FILING DATE: 23-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 854C1D2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 888 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-447-314-35

Query Match 0.5%; Score 57; DB 3; Length 888;
Best Local Similarity 23.3%; Pred. No. 6.4e+02;
Matches 14; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1210 ILELQHKKLESPVLTPIPNLSPTLPPQPGNMMETKGLISGLINICOKLSPD 1269
DB 752 IYDILQGNLKPQVDFLDGLIXLSMSRWELNDRDPSFAELREDLENTLKALPPAQEPD 811

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RESULT 136

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-08-970-264A-29

Query Match 0.5%; Score 57; DB 2; Length 2987;
Best Local Similarity 31.4%; Pred. No. 4.1e+03;
Matches 15; Conservative 6; Mismatches 29; Indels 0; Gaps 0.
QY 384 TKSLKRLNHLHLAGLFEYISYSSQFMDKNSKVSLLNQFLPLRLLES 434
DB 131 TNLTKRAHSALESFLKQVSMVADAFPHKKNKYQFMQDFYCTIENMDS 181

RESULT 139
US-09-407-562-29
Sequence 29, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION:
APPLICANT: Katchen, Mark
TITLE OF INVENTION: Genetic Test For Feline Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,407,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334 October 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DECKET NUMBER: 05860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 29.
SEQUENCE CHARACTERISTICS:
LENGTH: 2987 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562 29

Query Match 0.5%; Score 57; DB 4; Length 2987;
Best Local Similarity 31.4%; Pred. No. 4.1e+03;
Matches 19; Conservative 6; Mismatches 25; Indels 5; Gaps 0.

QY 384 TELSLENNIHLIASLFEYISYSSQFMDKNSKVSLLNQFLPLRLLES 434
DB 131 TNLTKRAHSALESFLKQVSMVADAFPHKKNKYQFMQDFYCTIENMDS 181

RESULT 140
US-07-925-695-8
Sequence 8, Application US/07925695
Patent No. 5428145
GENERAL INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMURA, Tetsuo
TITLE OF INVENTION: NON-P HEPATITIS VIRUS GENOME,
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
TITLE OF INVENTION: DETECTION SYSTEMS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi, Wellacher & Young
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
FILING DATE: 19920807
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 297402/91
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 360441/91
FILING DATE: 05-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DECKET NUMBER: 06,987-44009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-1462
TELEX: WHI 64470
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
US-07-925-695-8

Query Match 0.5%; Score 57; DB 1; Length 3033;
Best Local Similarity 38.5%; Pred. No. 4.2e+03;
Matches 10; Conservative 8; Mismatches 8; Indels 0; Gaps 0.

QY 1824 PAIKKTYKQIEFKNKNHMGPFMSHIQ 1849
DB 1752 PAIQSSWEKLEQFWAKHMMNFISGIQ 1777

RESULT 141
US-07-925-695-9
Sequence 9, Application US/07925695
Patent No. 5428145
GENERAL INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMURA, Tetsuo
TITLE OF INVENTION: NON-P HEPATITIS VIRUS GENOME,

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1  TITLE OF INVENTION: POLYPEPTIDES, ANTIBODIES, ANTIGENS, ANTIBODY AND
2  TITLE OF INVENTION: DETECTION SYSTEMS
3  NUMBER OF SEQUENCES: 9
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Boyer-Groff, Benjamin A.,
6  STREET: 1600 M Street, N.W., Suite 800
7  CITY: Washington
8  STATE: D.C.
9  COUNTRY: US
10 ZIP: 20004
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC DOS/MS DOS
15 SOFTWARE: Patent 15 Release #1.0, Version #1.05
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: 08/970,695
18 FILING DATE: 08/07/97
19 CLASSIFICATION: 445
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 08/287,402/91
22 FILING DATE: 08/01/91
23 PCT APPLICATION DATA:
24 APPLICATION NUMBER: 08/287,402/91
25 FILING DATE: 08/01/91
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Boyer-Groff, Benjamin A.
28 REGISTRATION NUMBER: 29,541
29 REFERENCE/BOOK NUMBER: 150
30 TELEPHONE: (202) 659,2811
31 TELEFAX: (202) 659,1432
32 FAX: 801,64176
33 INFORMATION FOR SEQ ID NO: 1:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 495 amino acids
36 TYPE: AMINO ACID
37 STRANDEDNESS: linear
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 HYPOTHETICAL: no
41 ANTI-SENSE: no
42 US-09-603-665-5

```

```

Query Match: 0.5%, Score 57, 10 2, Length 3033;
Best Local Similarity: 41.4%, Fied. No. 6, 20-03;
Matches: 16; Conservative 6; Mismatches 8; Gaps 0;

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1  16-24 PATENT 15 RELEASE #1.0, Version #1.05
2  11 11 11 11 11 11 11 11 11 11
3  1752 PATENT 15 RELEASE #1.0, Version #1.05

```

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RESULT 143

```

```

US-09-603-665-5
1  Sequence 30, Application US/09-603-665-5
2  Patent No. 6294334
3  GENERAL INFORMATION:
4  APPLICANT: Kathryn Meek
5  TITLE OF INVENTION: Genetic Test For Equine Severe
6  NUMBER OF SEQUENCES: 32
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Dr. Benjamin A. Adler
9  STREET: 8011 Candler Lane
10 CITY: Houston
11 STATE: Texas
12 COUNTRY: USA
13 ZIP: 77071
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: Macintosh
17 SOFTWARE: Microsoft Word for Macintosh
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: 08/970,695
20 FILING DATE: 08/07/97
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/287,402/91
23 FILING DATE: 08/01/91
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Adler Ph.D., Benjamin A.
26 REGISTRATION NUMBER: 35,423
27 REFERENCE/BOOK NUMBER: 150600
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 713-777-2321
30 TELEFAX: 713-777-6908
31 INFORMATION FOR SEQ ID NO: 30:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 3959 amino acid
34 TYPE: amino acid
35 STRANDEDNESS: linear
36 TOPOLOGY: linear

```

```

1  APPLICATION NUMBER: 08/970,695
2  FILING DATE: 08/07/97
3  CLASSIFICATION: 445
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Adler Ph.D., Benjamin A.
6  REGISTRATION NUMBER: 35,423
7  REFERENCE/BOOK NUMBER: 150600
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 713-777-2321
10 TELEFAX: 713-777-6908
11 INFORMATION FOR SEQ ID NO: 30:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 3959 amino acid
14 TYPE: amino acid
15 STRANDEDNESS: linear
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 HYPOTHETICAL: no
19 ANTI-SENSE: no
20 US-09-603-665-5

```

```

Query Match: 0.5%, Score 57, 10 2, Length 3959;
Best Local Similarity: 41.4%, Fied. No. 6, 20-03;
Matches: 16; Conservative 6; Mismatches 29; Gaps 0;

```

```

1  16-24 PATENT 15 RELEASE #1.0, Version #1.05
2  11 11 11 11 11 11 11 11 11 11
3  1752 PATENT 15 RELEASE #1.0, Version #1.05

```

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RESULT 143

```

```

US-09-603-665-5
1  Sequence 30, Application US/09-603-665-5
2  Patent No. 6294334
3  GENERAL INFORMATION:
4  APPLICANT: Kathryn Meek
5  TITLE OF INVENTION: Genetic Test For Equine Severe
6  NUMBER OF SEQUENCES: 32
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Dr. Benjamin A. Adler
9  STREET: 8011 Candler Lane
10 CITY: Houston
11 STATE: Texas
12 COUNTRY: USA
13 ZIP: 77071
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: Macintosh
17 SOFTWARE: Microsoft Word for Macintosh
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: 08/970,695
20 FILING DATE: 08/07/97
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/287,402/91
23 FILING DATE: 08/01/91
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Adler Ph.D., Benjamin A.
26 REGISTRATION NUMBER: 35,423
27 REFERENCE/BOOK NUMBER: 150600
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 713-777-2321
30 TELEFAX: 713-777-6908
31 INFORMATION FOR SEQ ID NO: 30:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 3959 amino acid
34 TYPE: amino acid
35 STRANDEDNESS: linear
36 TOPOLOGY: linear

```

MOLECULE TYPE: protein
HYPOTHETICAL: no
ANTI-SENSE: no
US-09-407-562-30

Query Match 0.5%; Score 57; DB 4; Length 3959;
Best Local Similarity 31.4%; Pred. No. 6.6e+03;
Matches 16; Conservative 29; Mismatches 29; Indels 0; Gaps 0;

QY 484 TSLTSLTLLHLLHLLASLFFFTTLYVSGGEMFSGKVSGLNINCHPTIFLLLS 434
DB 131 TITPTAASALFSTFLVSNVAVLAFHKKKKEGTFEFGVATIFRMLLS 121

RESULT 144
US-09-036-987A-5
Sequence 5, Application US/0903698/A
Patent No. 614526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
REGISTRATION NUMBER: 24,474
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4928 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-036-987A-5

Query Match 0.5%; Score 57; DB 4; Length 4928;
Best Local Similarity 27.8%; Pred. No. 8.6e+03;
Matches 10; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 633 LHPLKQWEALENVKSTPKGKLGIVANOKMIELL 668
DB 4887 LHALLAKWGAARDGTARATSPQSLTAATDDEIFDEI 4922

RESULT 145

US-09-370-700-5
Sequence 5, Application US/09370700
Patent No. 6274350
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT FILING DATE: 1999-08-09
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
TYPE: PRT
ORGANISM: Saccharopolyspora spinosa
US-09-370-700-5

Query Match 0.5%; Score 57; DB 4; Length 4928;
Best Local Similarity 27.8%; Pred. No. 8.6e+03;
Matches 10; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 633 LHPLKQWEALENVKSTPKGKLGIVANOKMIELL 668
DB 4887 LHALLAKWGAARDGTARATSPQSLTAATDDEIFDEI 4922

RESULT 146
US-09-100-804-20
Sequence 20, Application US/09100804
Patent No. 6066472
GENERAL INFORMATION:
APPLICANT: GOREZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLARSSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREFNFELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100.804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US44/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:


```

NAME: JAMES, EDWARD E.
REGISTRATION NUMBER: 1,616
PTEEN/REGISTRATION NUMBER: 2,147,088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 720-8510
TELEFAX: 617 720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 201
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROPHILICITY:
ANTISENSE: N
DB 001 100 004 20
Query Match
Best Local Similarity: 34.5%; Score 56; DB 4; Length 75;
Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
27 1821 VVPAIVYVQVIFKKNWKNHMDQSHQ 1849
1 111 111 1 1 1 1 1 1
DB 177 VGVAVGVNKKKLEFFWAKDMNPFSGIQ 205
RESULT 148
US-08-701-191A-21
Sequence 21, Application US/08701191A
Patent No. 5942428
GENERAL INFORMATION:
APPLICANT: Meesa Mohammadi, Joseph Schlossinger,
APPLICANT: and Steven R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
OF THE INVENTION, OF ROR INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: 1500 S Lyon
STREET: 63 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. Dots 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08701191A
FILING DATE: August 21, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 2,17,088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 455-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DB 001 101 191A 21
Query Match
Best Local Similarity: 33.4%; Score 56; DB 2; Length 290;
Matches 12; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
27 1210 ILELCQFFFI PSPQILVPTFTFNI SPQIVD PGP 1245
1 1 1 1 1 1 1 1 1 1 1 1
DB 256 IYDLEKGNRKKQADCLGALALN SROWELN QDK 271
RESULT 149
US-08-989-478-3
Sequence 3, Application US/08989478
Patent No. 5986082
GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle

```

APPLICANT: Stevens, Henry York
 APPLICANT: Ryals, John
 TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
 TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 5986082artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 5986082th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/08/989,478
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,177
 FILING DATE: 13-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,379
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,382
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,740
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,021
 FILING DATE: 10 JAN 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,022
 FILING DATE: 10 JAN 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Meligs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE NUMBER: 14,75-212147(1,000-1911)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO. 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 314 amino acids
 TYPE: amino acid
 STRANDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-989,478 3

Query Match 0.5%; Score 56; DB 2; Length 314;
 Best Local Similarity 25.4%; Pred. No. 1,86+02;
 Matches 15; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
 QY 445 EEHLEFFACKKQFTFQGFVSLSTSGKRYQFLADSDTSLMLSLNPIAPVRLAMNHILK 503
 DB 40 LHTLQWVKELELEQLQVLAALAAFTWKKQLTEHCDSFLHATLHEKPYDMEVIGQVK 98

RESULT 150
 US-08-996-685-3
 Sequence 3; Application US/08996685
 Patent No. 6031153
 GENERAL INFORMATION:
 APPLICANT: Ryals, John
 APPLICANT: Friedrich, Leslie
 APPLICANT: Okres, Scott

APPLICANT: Molina, Antonio
 APPLICANT: Ruess, Wilhelm
 APPLICANT: Krauf-Reiter, Gertrude
 APPLICANT: Kunt, Ruth
 APPLICANT: Kessmann, Helmut
 APPLICANT: Oostendorp, Michael
 TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6031153artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6031153th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,685
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/761,543
 FILING DATE: 6-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,378
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,379
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,382
 FILING DATE: 27-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/034,730
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,021
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,022
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/035,024
 FILING DATE: 10-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/875,015
 FILING DATE: 16-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Meligs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE NUMBER: 14,75-212147(1,000-1912)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO. 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 314 amino acids
 TYPE: amino acid
 STRANDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-996-685-3

Query Match 0.5%; Score 56; DB 3; Length 314;
 Best Local Similarity 25.4%; Pred. No. 1,86+02;
 Matches 15; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
 QY 445 EEHLEFFACKKQFTFQGFVSLSTSGKRYQFLADSDTSLMLSLNPIAPVRLAMNHILK 503

STATE: California


```

; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,540
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis R.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WSOPL11254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 695 1718
; TELEFAX: 206 224 0779
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US 08-537-540-4

Query Match 0.5%; Score 56; DB 2; Length 591;
Best Local Similarity 34.6%; Pred. No. 4.7e+02;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 732 LQKKKKKLESVITAVIPSEWLEL 757
DB 224 LVKQINLSSLEPALELTHRWQVM 249

RESULT 160
US-08-656-034-2
; Sequence 2, Application US/08/55534
; Patent No. 6015691
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: Yu, Xue Jie
; TITLE OF INVENTION: IMMUNODOMINANT 120 KDA SURFACE-EXPOSED
; TITLE OF INVENTION: ADHESION PROTEIN GENES OF EHRlichia
; TITLE OF INVENTION: CHAFFENSI
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Burke
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,034
; FILING DATE: Concurrently Retewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cordier, Timothy S.
; REGISTRATION NUMBER: 38,414
; REFERENCE/DOCKET NUMBER: CTS0151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-034-2

Query Match 0.5%; Score 56; DB 3; Length 628;
Best Local Similarity 37.5%; Pred. No. 5.2e+02;
Matches 15; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2095 KHWVLLFEETFLAFMENVGVHDEQKTKQVPTV 2135
DB 210 KEDFTVSQSPSEPFVAESVSKVEQETNEVLKLDQV 249

RESULT 161
US-08-190-802A-63
; Sequence 63, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: T0P1, Fig. 46
; US-08-190-802A-63

Query Match 0.5%; Score 56; DB 1; Length 713;
Best Local Similarity 32.5%; Pred. No. 6.3e+02;
Matches 13; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1159 EQVPIFLPPPPFAKPICTVQAKPKPKPKSKSPESVQF 1198
DB 78 KHLKLGEGQFDHQTASITVQKQKQKQKQKQKQKQKQ 117

RESULT 162

```

US-09-477-446-63
 : Sequence 6, Application US/08257073
 : Patent No. 6,242,444
 : GENERAL INFORMATION:
 : APPLICANT: Morison & Foster
 : APPLICANT: Morison & Foster
 : TITLE OF INVENTION: White-Lettered Populines and Uses
 : TITLE OF INVENTION: Throat
 : NUMBER OF SEQUENCES: 265
 : REFERENCE ADDRESS:
 : ADDRESS: Morison & Foster
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1942
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08257073
 : FILING DATE: 07 JUN 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/487,072
 : FILING DATE: 07 JUN 1995
 : APPLICANT: INF-EMAL-INC
 : NAME: MORISON, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/SEQUENCE NUMBER: 265000025-20
 : TITLE OF INVENTION: INF-EMAL-INC
 : TELEPHONE: (202) 607-1500
 : TELEFAX: (202) 607-0764
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 713 amino acids
 : TYPE: amino acid
 : P-CLASS: unknown
 : MOLECULE TYPE: protein
 : HYDROPHILIC: NO
 : ANTI-SENSE: NO
 : ORIGIN: SOURCE
 : INDIVIDUAL IS-GATE: 1001, F14, 46
 : US-09-477-446-63

Query Match: 0.5% Score 56; ID 4; Length 713
 Best Local Similarity: 31.7% Pred. No. 6,66e-02
 Matches: 13; Conservative: 11; Mismatches: 16; Gaps: 0;

US-09-477-446-63
 : Sequence 6, Application US/08257073
 : Patent No. 6,242,444
 : GENERAL INFORMATION:
 : APPLICANT: Morison & Foster
 : APPLICANT: Morison & Foster
 : TITLE OF INVENTION: White-Lettered Populines and Uses
 : TITLE OF INVENTION: Throat
 : NUMBER OF SEQUENCES: 265
 : REFERENCE ADDRESS:
 : ADDRESS: Morison & Foster
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1942
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08257073
 : FILING DATE: 07 JUN 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/487,072
 : FILING DATE: 07 JUN 1995
 : APPLICANT: INF-EMAL-INC
 : NAME: MORISON, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/SEQUENCE NUMBER: 265000025-20
 : TITLE OF INVENTION: INF-EMAL-INC
 : TELEPHONE: (202) 607-1500
 : TELEFAX: (202) 607-0764
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 713 amino acids
 : TYPE: amino acid
 : P-CLASS: unknown
 : MOLECULE TYPE: protein
 : HYDROPHILIC: NO
 : ANTI-SENSE: NO
 : ORIGIN: SOURCE
 : INDIVIDUAL IS-GATE: 1001, F14, 46
 : US-09-477-446-63

US-09-477-446-63
 : Sequence 6, Application US/08257073
 : Patent No. 6,242,444
 : GENERAL INFORMATION:
 : APPLICANT: Morison & Foster
 : APPLICANT: Morison & Foster
 : TITLE OF INVENTION: White-Lettered Populines and Uses
 : TITLE OF INVENTION: Throat
 : NUMBER OF SEQUENCES: 265
 : REFERENCE ADDRESS:
 : ADDRESS: Morison & Foster
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1942
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08257073
 : FILING DATE: 07 JUN 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/487,072
 : FILING DATE: 07 JUN 1995
 : APPLICANT: INF-EMAL-INC
 : NAME: MORISON, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/SEQUENCE NUMBER: 265000025-20
 : TITLE OF INVENTION: INF-EMAL-INC
 : TELEPHONE: (202) 607-1500
 : TELEFAX: (202) 607-0764
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 713 amino acids
 : TYPE: amino acid
 : P-CLASS: unknown
 : MOLECULE TYPE: protein
 : HYDROPHILIC: NO
 : ANTI-SENSE: NO
 : ORIGIN: SOURCE
 : INDIVIDUAL IS-GATE: 1001, F14, 46
 : US-09-477-446-63

US-09-477-446-63
 : Sequence 6, Application US/08257073
 : Patent No. 6,242,444
 : GENERAL INFORMATION:
 : APPLICANT: Morison & Foster
 : APPLICANT: Morison & Foster
 : TITLE OF INVENTION: White-Lettered Populines and Uses
 : TITLE OF INVENTION: Throat
 : NUMBER OF SEQUENCES: 265
 : REFERENCE ADDRESS:
 : ADDRESS: Morison & Foster
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1942
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08257073
 : FILING DATE: 07 JUN 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/487,072
 : FILING DATE: 07 JUN 1995
 : APPLICANT: INF-EMAL-INC
 : NAME: MORISON, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/SEQUENCE NUMBER: 265000025-20
 : TITLE OF INVENTION: INF-EMAL-INC
 : TELEPHONE: (202) 607-1500
 : TELEFAX: (202) 607-0764
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 713 amino acids
 : TYPE: amino acid
 : P-CLASS: unknown
 : MOLECULE TYPE: protein
 : HYDROPHILIC: NO
 : ANTI-SENSE: NO
 : ORIGIN: SOURCE
 : INDIVIDUAL IS-GATE: 1001, F14, 46
 : US-09-477-446-63

US-09-477-446-63
 : Sequence 6, Application US/08257073
 : Patent No. 6,242,444
 : GENERAL INFORMATION:
 : APPLICANT: Morison & Foster
 : APPLICANT: Morison & Foster
 : TITLE OF INVENTION: White-Lettered Populines and Uses
 : TITLE OF INVENTION: Throat
 : NUMBER OF SEQUENCES: 265
 : REFERENCE ADDRESS:
 : ADDRESS: Morison & Foster
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20006-1942
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08257073
 : FILING DATE: 07 JUN 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/487,072
 : FILING DATE: 07 JUN 1995
 : APPLICANT: INF-EMAL-INC
 : NAME: MORISON, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/SEQUENCE NUMBER: 265000025-20
 : TITLE OF INVENTION: INF-EMAL-INC
 : TELEPHONE: (202) 607-1500
 : TELEFAX: (202) 607-0764
 : INFORMATION FOR SEQ ID NO: 63:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 713 amino acids
 : TYPE: amino acid
 : P-CLASS: unknown
 : MOLECULE TYPE: protein
 : HYDROPHILIC: NO
 : ANTI-SENSE: NO
 : ORIGIN: SOURCE
 : INDIVIDUAL IS-GATE: 1001, F14, 46
 : US-09-477-446-63

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Journal of Management Inquiry 23(4) 401–417

ATTORNEY/AGENT INFORMATION:
 FILING DATE:
 NAME: WILSON M. LOCK, JR.
 REGISTRATION NUMBER: 35,067
 REFERENCE/AGENT NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-691-8895
 TELEFAX:
 INDEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1895 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROPHILIC:
 ANTI-SENSE:
 FRAGMENT TYPE:
 OPTIMAL SOURCE: spleen cell of homo sapiens

Query Match 0.5%; Score 56; DB 1; Length 1895;
 Best Local Similarity 47.5%; Pred. No. 2,760,04;
 Matches 12; Conservative 5; Mismatches 15; Indels 6; Gaps 0;

QY 1000 USNPERGVLQFLNCKYKFLFDLQHT 2011
 10 672 EKQFDLFACTLSHLEVEYKAVVETQKIV 600

RESULT 169
 US-08-619-554-4

Sequence 4, Application 35/8614554
 Patent No. 6,214,554
 GENERAL INFORMATION:
 APPLICANT: BOULGAS, Camille M.
 APPLICANT: CHERRIE, Gary L.
 APPLICANT: LEMAS, Joseph
 APPLICANT: ELSHERREINI, Mohammed
 APPLICANT: FOWE, Forrest
 APPLICANT: KAHN, Benjamin
 APPLICANT: KELLY, Rosamund
 APPLICANT: MARRINAN, Paul
 APPLICANT: MARRIN, Mary
 APPLICANT: ONISHI, Junji
 APPLICANT: SHELL, Gordon
 TITLE OF INVENTION: SYNTHETIC 1,3-BETA D GLUCAN
 TITLE OF INVENTION: SYNTHASE SUBUNIT
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 APPLICANT: JOSEPH A. MARRIN, 140
 STREET, 126 EAST LINDEN AVENUE - P.O. BOX 2009
 CITY: RAHWAY
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Windows Version 3.0
 SOFTWARE: FASTSEQ for Windows
 PRIOR APPLICATION NUMBER: 35/861454
 FILING DATE: 01 AUG-1996
 CLASSIFICATION: C06
 APPLICATION NUMBER: 35/861454
 FILING DATE: 01 SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON M. LOCK, JR.
 REGISTRATION NUMBER: 35,067
 REFERENCE/AGENT NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-691-8895
 TELEFAX:
 INDEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1895 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

REFERENCE/AGENT NUMBER: 1910451
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 742-594-6734
 TELEFAX: 742-594-4720
 INDEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1895 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-619-554-4

Query Match 0.5%; Score 56; DB 2; Length 1895;
 Best Local Similarity 24.2%; Pred. No. 2,800,04;
 Matches 16; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 745 VELWAHYVEELNSTQPVAVDSVFLVSEKFTLYALKAHRSFPELHWNIQELFUSKO 624
 10 645 LDKWSYVWVIVFAAKYAESYFELLSLELDTFELLSLSMSYTFYWWNFYVJPEI 644

QY 825 YHLLI 840
 DB 695 VLGLMI 700

RESULT 169
 US-08-596-291-3

Sequence 4, Application 35/08596291
 Patent No. 5,821,075
 GENERAL INFORMATION:
 APPLICANT: GORTZ, LIGREL JORGE
 APPLICANT: SARAS, JAN
 APPLICANT: CLAESSON-WELSH, LENA
 APPLICANT: HELDIN, CARL-HENRIK
 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
 TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NEW PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 APPLICANT: WOLF, GREENFIELD & SACKS, P.C.
 STREET: 600 ATLANTIC AVENUE
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PLOTCH; POLYSE #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/596,291
 FILING DATE: 09-AUG-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/ 15,574
 FILING DATE: 01-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: GATES, EDWARD R.
 REGISTRATION NUMBER: 31,616
 REFERENCE/AGENT NUMBER: 04617000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/720-4500
 TELEFAX: 617/720-2441
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2465 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-552-1

Query Match 0.5%; Score 56; DB 1; Length 3011;
Best Local Similarity 34.6%; Pred. No. 5,7e+03;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1821 VLLPAIKKTYQIEKNNKNNHMPMS 1846
1: 111: 333: 1 11 1:1
Db 1745 VITPAVOTNWKLEAFWAKHWNFI 1770

RESULT 176
US-08-710-637-1
Sequence 1, Application US/08/10637
Patent No. 5854001
GENERAL INFORMATION:
APPLICANT: CASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,637
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/144,099
FILING DATE:
APPLICATION NUMBER: US/07/830,024
FILING DATE: 01-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-710-637-1

Query Match 0.5%; Score 56; DB 2; Length 3011;
Best Local Similarity 34.6%; Pred. No. 5,7e+03;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1821 VLLPAIKKTYQIEKNNKNNHMPMS 1846

Db 1745 VITPAVOTNWKLEAFWAKHWNFI 1770
1: 111: 333: 1 11 1:1

RESULT 177
PCT-US93-00907-1
Sequence 1, Application PCT/US93/00907
GENERAL INFORMATION:
APPLICANT: CASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00907
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
TYPE: AMINO ACID
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-00907-1

Query Match 0.5%; Score 56; DB 5; Length 3011;
Best Local Similarity 34.6%; Pred. No. 5,7e+03;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1821 VLLPAIKKTYQIEKNNKNNHMPMS 1846
1: 111: 333: 1 11 1:1
Db 1745 VITPAVOTNWKLEAFWAKHWNFI 1770

RESULT 178
PCT-US94-07280-1
Sequence 1, Application PCT/US94/07280
GENERAL INFORMATION:
APPLICANT: WATANABE, SHINICHI
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: ONE ARBOL PARK ROAD
 CITY: ARBOL PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60943-6001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 09-AUG-1991
 CLASSIFICATION:
 APPLICANT: NAKAMURA, Hiroaki
 NAME: P. REMSKI, PRISCILLA F.
 REGISTRATION NUMBER: 33,207
 PREFERRED FILING NUMBER: 5521 no. 01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-947-6465
 TELEFAX: 708-948-2624
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3011 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 POT-0595-01087-1

Query Match: 0.53, Score 56, 104 1, Length 4011;
 Best Local Similarity: 34.6%, Pred. No. 5, 7e+04;
 Matches: 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

27 1821 VLPAIKTKYKTEFNWNNHMPMS 1846
 1 111 1111 1 1 111
 DE 1745 VITPAVITNWKLEAFWAMWNPIS 1770

RESULT 1:
 POT-0595-01087-1
 Sequence 1, Application US/07059501087
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, Hiroaki
 NAME: P. REMSKI, PRISCILLA F.
 REGISTRATION NUMBER: 33,207
 PREFERRED FILING NUMBER: 5521 no. 01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-947-6465
 TELEFAX: 708-948-2624
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3011 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 POT-0595-01087-1
 Query Match: 0.53, Score 56, 104 1, Length 4011;
 Best Local Similarity: 34.6%, Pred. No. 5, 7e+04;
 Matches: 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

TELEFAX: 708-948-2624
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3011 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 POT-0595-01087-1

Query Match: 0.53, Score 56, 104 1, Length 4011;
 Best Local Similarity: 34.6%, Pred. No. 5, 7e+04;
 Matches: 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

27 1821 VLPAIKTKYKTEFNWNNHMPMS 1846
 1 111 1111 1 1 111
 DE 1745 VITPAVITNWKLEAFWAMWNPIS 1770

RESULT 180
 US-07-925-695-5
 Sequence 5, Application US/07925695
 Patent No. 5428145
 GENERAL INFORMATION:
 APPLICANT: OKAMOTO, Hiroaki
 NAME: NAKAMURA, Tetsuo
 TITLE OF INVENTION: NON-A, N-N-B HEPATITIS VIRUS GENOME
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
 DETECTION SYSTEMS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: Beverly, Degrad, Weillacher & Young
 STREET: 1850 M Street, N.W., Suite 800
 CITY: Washington
 STATE: D.C.
 COUNTRY: US
 ZIP: 20046
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 03-07-1995, 695
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICANT NUMBER: JP 66141/91
 FILING DATE: 03-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Weillacher, Robert G.
 REGISTRATION NUMBER: 20,531
 TELEPHONE: (202) 659-2811
 TELEFAX: (202) 659-1462
 TELEFAX: W01 64470
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4033 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 POT-07-925-695-5

Query Match: 0.53, Score 56, 104 1, Length 4033;
 Best Local Similarity: 34.6%, Pred. No. 5, 7e+04;
 Matches: 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

100


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1 COUNTRY: United States of America
2 ZIP: 60606-6402
3
4 MEDIUM READABLE FORM:
5 MEDIUM TYPE: floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC DOS/MS-DOS
8 SOFTWARE: Patent In Release #1.0, Version #1.25
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: 05/006,156
12 FILING DATE:
13 CLASSIFICATION:
14
15 FRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 05/075,117
17 FILING DATE: 20-APR-1990
18
19 ALLOWED/ADMIN INFORMATION:
20 NAME: Clough, David W.
21 REGISTRATION NUMBER: 36,137
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 312/471-6332
24 TELEFAX: 312-474-0448
25 TELEX: 25-0656
26
27 INFORMATION FOR SEQ ID NO: 85:
28 SEQUENCE CHARACTERISTICS
29 LENGTH: 734 amino acids
30 TYPE: amino acid
31 topology: linear
32
33 MOLECULE TYPE: protein
34
35 NAME/KEY: misc-feature
36 OTHER INFORMATION: Note "Sequence corresponds to peptide
37 Patent No. 6,069,240
38
39 OTHER INFORMATION: acids 152-885 of SEQ ID NO:22 which begins immediately after
40 OTHER INFORMATION: codon. Stop codon may be in an intron."
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42 US-05-146-249A-85
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Query Match 0.5%, Score 55; DB 1; Length 857;
 Best Local Similarity 38.2%; Pred. No. 1,26,03;
 Matches 13; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 592 LKKIMTKSKCVDSPIKEAVIARIGRHHIUVL 535
 III III III : : III I I
 DB 555 VKRIKTSVQGTDFEMNEVTLIARLQHINLVQVL 588

RESULT 192
 US-08-474-379C-65
 ; Sequence 65, Application US/08474379C
 ; Patent No. 6067795
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 ; STREET: 233 South Wacker Drive/6400 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/206,188
 ; FILING DATE: 01-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/688,352
 ; FILING DATE: 14-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 886 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-474-379C-65

Query Match 0.5%, Score 55; DB 2; Length 886;
 Best Local Similarity 40.0%; Pred. No. 1,26,03;
 Matches 13; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 592 PLVQIENPIAGCPPEPVTHIIPCTAQ 2051
 III I I III I I I I
 DB 702 PLPQKQPELITPEEPFISMAIIPCTAQ 731

RESULT 193
 US-09-146-249A-65
 ; Sequence 55, Application US/09046249A
 ; Patent No. 6069240

GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 ; STREET: 6400 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,249A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 65:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 886 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-146-249A-65

Query Match 0.5%, Score 55; DB 3; Length 886;
 Best Local Similarity 40.9%; Pred. No. 1,26,03;
 Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2022 PLVQIENPIAGCPPEPVTHIIPCTAQ 2051
 III I I III I I I I
 DB 702 PLPQKQPELITPEEPFISMAIIPCTAQ 731

RESULT 194
 US-08-206-188B-65
 ; Sequence 65, Application US/08206188B
 ; Patent No. 6100025
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 ; STREET: 6400 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715
FILING DATE: 01-MAR-1994
CLASSIFICATION: 455
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cloud, David W.
REGISTRATION NUMBER: 66107
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 200486
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 09-603-665-5

Query Match 0.58; Score 55; DB 4; Length 886;
Best local similarity 40.08; Pred. No. 1,20+03;
Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Q7 2022 FLVQLERLNGSEPKFQPVTVKILPCTAQ 2051
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DB 702 PLPDKFQFELILEEEEEELISMAQ PCTAQ 705

RESULT 195

US 09-603-665-5
Sequence 12, Application US/09474-249A
Patent No. 6069240

GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 South Wacker Drive/6300 South Wacker Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 07-JUN-1995

CLASSIFICATION: 455

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,188
FILING DATE: 01-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,462
FILING DATE: 19-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Cloud, David W.

REGISTRATION NUMBER: 66,107

REFERENCE: 5,115,300; 5,115,301; 5,115,302

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08-474-379C 12

Query Match 0.58; Score 55; DB 2; Length 898;
Best local similarity 40.08; Pred. No. 1,20+03;
Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Q7 2022 FLVQLERLNGSEPKFQPVTVKILPCTAQ 2051
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DB 676 PLPDKFQFELILEEEEEELISMAQ PCTAQ 705

RESULT 196

US 09-146-249A-12
Sequence 12, Application US/09146-249A
Patent No. 6069240

GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 South Wacker Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/46,249A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990

ATTORNEY/AGENT INFORMATION:
NAME: Cloud, David W.

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 09-146-249A-12

Query Match 0.58; Score 55; DB 4; Length 898;
Best local similarity 40.08; Pred. No. 1,20+03;
Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Q7 2022 FLVQLERLNGSEPKFQPVTVKILPCTAQ 2051
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DB 676 PLPDKFQFELILEEEEEELISMAQ PCTAQ 705

RESULT 197

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US-08-206-188B-12
? Sequence 12, Application US/08206188B
? Patent No. 6100025
? GENERAL INFORMATION:
? APPLICANT: Widler, Michael H.
? ADDRESSEE: Colicelli, John J.
? TITLE OF INVENTION: Cloning by Complementation and Related
? NUMBER OF SEQUENCES: 84
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borin
? STREET: 6300 Sears Tower, 233 South Wacker Drive
? CITY: Chicago
? STATE: Illinois
? COUNTRY: United States of America
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1 0, Version #1 35
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/206,188B
? FILING DATE: 01-MAR-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/511,715
? FILING DATE: 20-APR-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Crough, David W.
? REGISTRATION NUMBER: 36137
? TELEPHONE: 312 474-6400
? TELEFAX: 312 474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 12:
? LENGTH: 898 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-206-188B-12

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Query Match 0.5%; Score 55; DB 3; Length 898;
Best local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0.

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QY 2022 PLVQKQFELTLEEEEREISMAQJPCQA 2051
Db 676 PLVQKQFELTLEEEEREISMAQJPCQA 705

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RESULT 194
US-07-688-352C-12
? Sequence 12, Application US/07688352C
? Patent No. 5525996
? GENERAL INFORMATION:
? APPLICANT: Widler, Michael H.
? ADDRESSEE: Colicelli, John J.
? TITLE OF INVENTION: Cloning by Complementation and Related
? NUMBER OF SEQUENCES: 57
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
? ADDRESSEE: Ricknell
? STREET: Two First National Plaza, 20 South Clark
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60602
? COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1 0, Version #1 25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/688,352C
? FILING DATE: 19910419
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/511,715
? FILING DATE: 20-APR-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Boron, Michael F.
? REGISTRATION NUMBER: 25447
? REFERENCE/DOCKET NUMBER: 27805/30197
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 346-5750
? TELEFAX: (312) 984-9740
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 900 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-07-688-352C-12

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Query Match 0.5%; Score 55; DB 1; Length 900;
Best local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

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QY 2022 PLVQKQFELTLEEEEREISMAQJPCQA 2051
Db 678 PLVQKQFELTLEEEEREISMAQJPCQA 707

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RESULT 199
US-08-968-752B-6
? Sequence 6, Application US/08968752B
? Patent No. 6043073
? GENERAL INFORMATION:
? APPLICANT: Frohman, Michael A.
? APPLICANT: Morris, Andrew
? TITLE OF INVENTION: DNA Sequences
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: GNYX Pharmaceuticals, Inc.
? STREET: 3031 Research Drive
? CITY: Richmond
? STATE: California
? COUNTRY: USA
? ZIP: 94806
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1 0, Version #1 30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/968,752B
? FILING DATE: 13-AUG-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/025,469
? FILING DATE: 05-SEP-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Giotta, Gregory J.
? REGISTRATION NUMBER: 32,028
? REFERENCE/DOCKET NUMBER: GNYX2004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 510 222-9700
? TELEFAX: 510 222-9758

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Search completed: November 6, 2001, 12:20:56
Job time: 254 sec

1 INFORMATION FOR SEQ ID NO: 61
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 552 amino acids
4 TYPE: amino acid
5 topology: linear
6 MOLECULE TYPE: protein
7
8 US 09 603 665 B-6

Query Match: 0.562 Score 55: DB 4: Length 942:
Best Local Similarity: 26.003 P-Id: 1.00004:
Matches: 143 Conservative: 83 Mismatches: 29: Indels: 0: Gaps: 0:

27 143 VENVVHSHSEKREHREKLSVEMSCGLSSNNEKEVVSQDEIKELKE 1619

46 622 LINAVALHRESQHFYENFFISSTGRIVEKNGVDEIVRIKAEHC 671

RESULT: 260

DB: 09 540 005

Sequence 7: Application: US/08560005

Patent No.: 6,184

GENERAL INFORMATION:

APPLICANT: PDI, David A.

APPLICANT: Williams, Lewis I.

APPLICANT: Patterson, Anne Bennett

APPLICANT: Maples, Philip W.

TITLE OF INVENTION: No. 60016441 GR02 Association Protein and Nucleic

TITLE OF INVENTION: Acidic Encoding Thereof

NUMBER OF SEQUENCES: 10

REFERENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew

STREET: 100 Market Plaza, Stuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

SEQUENCE FEATURES:

METHOD: EMBOSS

METHOD: EMBOSS

SOFTWARE: EMBOSS/MS 1.0, Version #1.25

SOFTWARE: EMBOSS/MS 1.0, Version #1.25

APPLICATION DATA:

APPLICATION NUMBER: US/08/560,005

FILING DATE:

CLASSIFICATION: 4.05

ALL PREVIOUS INFORMATION:

NAME: David A. Williams

REFERENCE NUMBER: 26.003

REFERENCE/SEQUENCE NUMBER: 26.003

REFERENCE/SEQUENCE NUMBER: 26.003

REFERENCE/SEQUENCE NUMBER: 26.003

REFERENCE/SEQUENCE NUMBER: 26.003

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Watanabe M., Hoshino T., Kato Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Uno Y., Takiguchi S.,
Watanabe G., Kimura K., Moriyama K., Ishii S., Kawai Y., Saito K.,
Yamamoto T., Wakamatsu A., Nakamura Y., Nagahara K., Masuko Y.,
Ninomiyi K., Iwayanagi T.,
"NEDO human cDNA sequencing project",
Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AK001221; BAA01564.1; -
SEQUENCE: 349 AA; 40626 MW; 6061420AA; 6665; 67644;

Query Match 16.5%; Score 1778; DB 4; Length 349;
Best local Similarity 99.1%; Pred. No. 2, 9a-221;
Matches 346; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1796 MGSASQANIPITSLKRTATLADPVIIPATKIKYAGIKKRNKHMSPFMSIIQEHIGVM 1855
|||||
1 MGSASQANIPITSLKRTATLADPVIIPATKIKYAGIKKRNKHMSPFMSIIQEHIGVM 60
1856 KKEELISGSGTATFLEALDPAGHSENIIEVQKTFNCLIPVAMVVKISPVTFRPL 1915
|||||
61 KKEELISGSGTATFLEALDPAGHSENIIEVQKTFNCLIPVAMVVKISPVTFRPL 120
1916 PKKLTWAKTDAPKDLITFNELAPKIKGLPTFGAGHVKVPFADTLXOVNISKTD 1975
|||||
121 PKKLTWAKTDAPKDLITFNELAPKIKGLPTFGAGHVKVPFADTLXOVNISKTD 180
1976 KAITUSRDERKGLLQGLLELYKELFUTGRRISKEPAXAIIMPIVQIEFRIGSFE 2035
|||||
181 EAFDSERIEKGLLQGLLELYKELFUTGRRISKEPAXAIIMPIVQIEFRIGSFE 240
2036 KTGKFFVTHITVIAQFSVAMAMISWFTNYGILKTPDSRPVPAALITVIALAKFL 2095
|||||
241 KTGKFFVTHITVIAQFSVAMAMISWFTNYGILKTPDSRPVPAALITVIALAKFL 300
2096 KENYVILIPESIPETAFIMETDPEFPHQCKTQIQITVIVLGRPLQSYF 2144
301 KENYVILIPESIPETAFIMETDPEFPHQCKTQIQITVIVLGRPLQSYF 349

RESULT 4
Q4VM75 PRELIMINARY: PRT: 2096 AA
ID Q4VM75
AC Q4VM75
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE G310805 PROTEIN.
GN G310805
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musciforma;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amannatides P.C., Scheraga S.F., Li P.W., Hinkins P.A., Galie P.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Mortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.R.C., Blazek R.C., Champs M., Pfeiffer R.D.,
Wan K.H., Boyle C., Haxel E.J., Holt R.A., Nelson M.W., Miklos G.L.G.,
Abriil J.P., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck D., Brckstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dalila C., Davenport I.A., Davies P.,
de Pablos B., Delcher A., Deng X., Mays A.D., Dew I., Dietz S.M.,
Fadison K., Foup L.E., Downes M., Dudan-Rocha S., Dunkov R.C., Dunn P.,
Durbin K.J., Evangelista C.C., Faraz C., Ferreira S., Fleischmann W.,

Foster C., Gabriellian A.E., Gaty N.S., Gelbart W.M., Glasser K.,
Gledok A., Gong F., Gorrrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Hattay B., Heiman J.J., Hernandez J.P., Hirsch J.,
Jalali M., Houston K.A., Howland T.J., Wei M.H., Ibequm C.,
Kimmel B.E., Kodira G.D., Kratt C., Kravitz S., Kuip D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Neison D.K., Nelson K.A., Nixon K., Nusskern D.P., Paclele J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Paine K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue H.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
Svirskas P., Teeter C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yen K.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou L.,
Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
Science 287:2185-2195 (2000).
RL EMBL: AB03615; AA052447.2;
DR FlyBase; FBN000164; G310805;
DR InterPro; IPR001395;
DR LocusTag; LOC001395;
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1;
DR SIGNIF 2016 AA, 257217 MW, 3E7PAC677PAPPP20 CP0664;

Query Match 4.7%; Score 511; DB 5; Length 2076;
Best local Similarity 48.0%; Pred. No. 6, 3e-56;
Matches 96; Conservative 39; Mismatches 65; Indels 0; Gaps 0;
2 TSLAQGLQALPAGASGASUSRDEVASLLEDFEKEAAI LKNDIAIAGCTGLEELIIFTS 51
|||||
3 TALAQLQALPAGASGASUSRDEVASLLEDFEKEAAI LKNDIAIAGCTGLEELIIFTS 52
62 FEQEPALPISQAKTIFPSVQTKAVNKQIDENISLILHLSPYELKPKAQKLEWLIHRF 121
|||||
63 FEQEPALPISQAKTIFPSVQTKAVNKQIDENISLILHLSPYELKPKAQKLEWLIHRF 172
122 HTHLYNQSLIACVLPYHPTFIVAVTQILKLNNSKRWFWLLPVKQSGVPLAKGTILITH 181
|||||
123 QVHEYNPSSEVMALILPYHPTFIVAVTQILKLNNSKRWFWLLPVKQSGVPLAKGTILITH 182
182 CYKDLQPMDFICSLVTSYK 201
183 AASNPATFICGQSTQKAVK 202

RESULT 5
O60179 PRELIMINARY: PRT: 1649 AA.
ID O60179
AC O60179
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL: 186.4 KDa Protein (449, 449 IN CHROMOSOME 11.
GN SPBC23E6.04C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Pohl T.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: TO YEAST YJL109C.

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16 EMBL: A002520.1; CAA18872.1;
17 GenBank: U00004.1;
18 Protein: p500077; GenBank: U00004.1
19 Hypothesized protein: Transmembrane
20 TRANSMEM 254 274 19181AA
21 DOMAIN 254 274 19181AA
22 SEQUENCE 1649 AA; 166409 MW; 6B4D0712521649 CR664;

Query Match:
Best Local Similarity 45.9%; Pred. No. 15;
Matches 43; Conservative 21; Mismatches 57; Indels 0; Gaps 0;

Q7 26 SLTPDRAAATVIRHDAVAGVGLRLLGHPSEQFAKLESIAKTLRSVATKAVN 87
100 IIIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 26 SLTPDRAAATVIRHDAVAGVGLRLLGHPSEQFAKLESIAKTLRSVATKAVN 87
100 IIIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Q7 88 FQNTSIFELHSEVLEFAPGFLFELWLRGPHLYNLSIAVLYVDFEFVAV 147
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 88 FQNTSIFELHSEVLEFAPGFLFELWLRGPHLYNLSIAVLYVDFEFVAV 147
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Q7 148 I 148
10 148 I 148
10 148 I 148

RESULT 6
Q24495
ID Q24495 PRELIMINARY: PRI: 1650 AA.
AC Q24495
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CODED FOR BY C. ELEPHANS (CNA YK08H3.5).
GN ZK430.1.
OS Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditidae.
OC Rhabditidae; Polychetidae; Caenothabditis.
OX NCBI_TaxID=6249;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE 94150718; PubMed 7406498;
RA Wilson R., Ainsworth R., Anderson K., Baynes C., Berks M.,
RA Wallfield J., Burton J., Connell M., Cooper J., Coulson A.,
RA Craxton M., Dear S., De Zee, Durbin R., Favallo A., Fulton L.,
RA Gardner A., Green P., Hawkins J., Hillier L., Hjer M., Johnston L.,
RA Jones M., Karslaw J., Kingston L., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riffon J., Roopra A., Saunders D., Showkoon P.,
RA Smalldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thirry Mier J., Thomas K., Vardoll M., Vardoll P., Watkinson P.,
RA Watson A., Weinstock J., Wilkins S., Woodhead P.,
RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RA elephas.*
RI Nature 368:32-36(1994).
RN 121
RP SEQUENCE FROM N.A.
RA Johnson J.
RI Submitted (Jan 1996) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RA Watson R.
RI Submitted (Dec 1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: 042633; AAA8061.1; -
DR GenBank: U00004.1; -
DR EMBL: U00004.1; -
DR EMBL: F50043; HHH_GNR_FAMILY; UNKN:WN1.
DR PROSITE: P50043; THIO-PROTEASIN; UNKN:WN1.
SQ SEQUENCE 1650 AA; 165226 MW; A414378F749F29 CR664;

Query Match:
Best Local Similarity 1.54%; Score 16.0; DB 5; Length 1650;
Matches 18; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

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Matches 31; Conservative 24; Mismatches 44; Indels 0; Gaps 0;

Q7 64 QFADPESAKTIPSVQVFAVNFQDENTISFTTHISVFLFKAGKGLFWLHREHI 124
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 64 QFADPESAKTIPSVQVFAVNFQDENTISFTTHISVFLFKAGKGLFWLHREHI 124
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Q7 124 HLYRQSSLIACVLPHYHETRFVAVIQLL 151
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 124 HLYRQSSLIACVLPHYHETRFVAVIQLL 151
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Q7 125 YSNAAETLLITLPPHETKIVYSKLRIL 152
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 125 YSNAAETLLITLPPHETKIVYSKLRIL 152
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII

RESULT 7
Q9P7M8
ID Q9P7M8 PRELIMINARY: PRI: 1564 AA.
AC Q9P7M8
DI 01-031-2000 (TREMBLrel. 15, Created)
DI 01-031-2000 (TREMBLrel. 15, Last sequence update)
DI 01-031-2000 (TREMBLrel. 15, Last annotation update)
DE NUCLEOPORIN.
GN NOP184.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=972H-7;
RA Soeder K., Harris D., Lyne M., Rajandream M.A., Barrell H.G.;
RI Submitted (Feb 2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL157917; CAB76031.1; -
KW Porin.
SQ SEQUENCE 1564 AA; 176062 MW; 248P7AFF39C70E7 CR664;

Query Match:
Best Local Similarity 0.7%; Score 76; DB 3; Length 1564;
Matches 18; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Q7 1709 NVLGSALLCICAEVISTILEALAPQPSLMPSILLIMKN1SLIV 1751
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 1709 NVLGSALLCICAEVISTILEALAPQPSLMPSILLIMKN1SLIV 1751
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Q7 886 NCLPRLCTAPILQILSALITAFNPSTPSTIAYMINSTDIV 928
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
10 886 NCLPRLCTAPILQILSALITAFNPSTPSTIAYMINSTDIV 928
100 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII

RESULT 8
Q9Y8G4
ID Q9Y8G4 PRELIMINARY: PRI: 1628 AA.
AC Q9Y8G4
DI 01-NOV-1999 (TREMBLrel. 12, Created)
DI 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DI 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NUCLEOPORIN.
GN NOP184.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE-95318F21; PubMed-10488805;
RA Whalen W.A., Yoon J.H., Shen R., Dhar R.;
RI "Regulation of mRNA export by nutritional status in fission yeast.";
RI Genetics 152:827-838(1999);
DR EMBL: AF055035; AAU44830.1; -
KW Porin.
SQ SEQUENCE 1628 AA; 184236 MW; AEC72819EFF40DB7 CR664;

Query Match:
Best Local Similarity 0.7%; Score 76; DB 3; Length 1628;
Matches 18; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

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RESULT 15
Q9H319 PRELIMINARY: PRT: 470 AA.
ID Q9H319
AC Q9H319
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MUTANT DESMIN
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID: 9606;
RN 111
RP SEQUENCE FROM N.A.
PA Park K.-Y., Palakas M.C., Semino-Mora C., Lee H.-S., Litvak S.,
PA Goldfarb D.G.;
PA Submitted (06-1999) to the EMBL/GenBank/DDBJ databases.
BL EMBL: AF167579; AAG41217.1;
FR VARIANT 406 406 W 12 K.
DE SEQUENCE 470 AA; 53565 MW; 1C2AEFAE4B4B8319 CRC64;
SQ
Query Match 0.7%; Score 73; DB 4; length 470;
Best Local Similarity 30.7%; Prod. No. 8.2;
Matches 23, Conservative 12; Mismatches 40; Indels 0; Gaps 0;
QY 2065 LNYQULLETHSSPKVFEALITVALAEFKENYIVLIPSTETFLAFMDPTFEVEHQ 2124
DB 194 LQELGOLKEAENLAAFRADVDAATLARIDLEKRLSUNFEAFILKKVIEELRELQAO 253
QY 2125 QKRTGQLEFVIGEP 2139
DB 254 LQPGVGVEMDMSKP 268
RESULT 16
ID Q83778 PRELIMINARY: PRT: 490 AA.
AC Q83778
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE SERINE-TYPE D-ALA-D-ALA CARBOXYPEPTIDASE (DACC).
GN TP0800.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema
OC NCBI_TaxID: 160;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE: 98332770; PubMed-9669870;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton K., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artach P., Bowman K., Colton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sadowsky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
RC spirochete";
RL Science 281:375-388(1998).
DR EMBL: AEO1251; AAC65769.1;
DR MEROPS: S11.001;
DR TIGR: TP0800;
DR InterPro: IP001967;
DR Pfam: PF00768; Peptidase S11; 1.
DR PRINTS: PR09725; DALACPTASEL.
DR Carboxypeptidase.
KW SEQUENCE 490 AA; 52809 MW; 7289A98ACEFACE3 CRC64;
Query Match 0.7%; Score 73; DB 2; length 490;

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Best Local Similarity 33.3%; Prod. No. 8.6;
Matches 25; Conservative 9; Mismatches 41; Indels 0; Gaps 0;
QY 291 TKIFSLIKDGLSCLIVLLGRQKPEISLGKKPFPHLCNVPDLITILHGISYTVDSPLLRYM 350
DB 370 TDVETALSDALPCAPVLGSKRGALRPILHPSTCTSCPVLTNPCTRTISITFALPPLLRAP 429
QY 351 LPHLVVSIHHVTGE 365
DB 430 LQETDVIGFARHLDE 444
RESULT 17
Q9YVT6 PRELIMINARY: PRT: 1127 AA.
ID Q9YVT6
AC Q9YVT6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
DE OFF-MSV155 HYPOTHETICAL PROTEIN
GN MSV155.
OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OC NCBI_TaxID: 83191;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-TUCSON;
RX MEDLINE: 99102412; PubMed-9847359;
RA Afonso C.L., Tulman E.R., Lu Z., Oma F., Kutish G.F., Rock D.L.;
RA "The genome of Melanoplus sanguinipes entomopoxvirus";
RL J. Virol. 73:533-552(1999).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN-TUCSON;
RA Afonso C.L., Tulman E.R., Lu Z., Oma F., Kutish G.F., Rock D.L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF064860; AAC97677.1;
SQ SEQUENCE 1127 AA; 134265 MW; F185DALD5A3FE7D1 CRC64;
Query Match 0.7%; Score 73; DB 14; length 1127;
Best Local Similarity 21.3%; Prod. No. 92;
Matches 19, Conservative 22; Mismatches 48; Indels 0; Gaps 0;
QY 1461 GSENNILQYLLKPEEKDETPKAVSPNKSEQEMLOVENVETHTSKLRHFKFLSVSE 1520
DB 164 ELLLELLKLVSSLSKSLFGLYKHHHFFLEPKRDLRVKLLHREGLDFGLFFS 223
QY 1521 MSOLLSSNNFLKVVESGGPRLKGLPER 1549
DB 124 EKLIFFQEEELNFTIFEEQENIRKFNOR 250
RESULT 18
ID Q73587 PRELIMINARY: PRT: 455 AA.
AC Q73587
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DESMIN.
OS Scyllorhinus stellaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes.
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyllorhinidae; Scyllorhinus.
OC NCBI_TaxID: 68454;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Schultess J., Loebbecke A., Schaffeld M., Lieb B., Markl J.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY.

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[illegible]

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.
 RC STRAIN-LANUSBERG ERECTA; TISSUE=FLOWER;
 RA Colter M.E., Saunders M.J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF004556; AAC01202.1;
 SQ SEQUENCE 275 AA; 32273 MW; ED06626256E576A5 FRC64;

Query Match 0.6%; Score 69; DB 10; Length 275;
 Best Local Similarity 23.9%; Pred. No. 15;
 Matches 17; Conservative 21; Mismatches 33; Indels 0; Gaps 0;
 QY 1217 KFFIPSPQIIIVPTLFIISQCFPIPGDFNMETKGTIIISGLINICQKISDYGCKIPKD 1276
 DB 43 EETLEKFTVTETKMPVLINIERILNAGCSMESSIISLINAMFHLERQVSDGIECPG 102
 QY 1277 ILDEKFNVEL 1287
 DB 103 VLTVDKIKFEL 113

RESULT 29 083089 PRELIMINARY; PRT: 202 AA.
 ID 083089;
 AC 083089;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN TP00050.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 NCBI_TaxID=160;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 Dodson R., Gwinn M., Hickley E.K., Clayton R., Ketchum K.A.,
 Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 McDonald L., Artach P., Rowman C., Cotton M.D., Fujii C., Garland S.,
 Hatch K., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 Venter J.C.;
 RL "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete."
 RL Science 281:375-388(1998).
 DR EMBL: AE001190; AA065046.1;
 DR TIGR: TP0050;
 DR InterPro: IPR000836;
 DR Pfam: PF00156; Pribosyltran; 1.
 KW Transferase.
 SQ SEQUENCE 202 AA; 23208 MW; F703AF702AR991UA CRC64;

Query Match 0.6%; Score 68; DB 2; Length 262;
 Best Local Similarity 27.4%; Pred. No. 14;
 Matches 26; Conservative 12; Mismatches 41; Indels 0; Gaps 0;

QY 749 KLESVITAVELPSEWHIEIMIDRGIPVELMAHYVELINSTORVAVESVFLVFLSKFTY 798
 DB 55 KAPPTIYAAVVAASHTLPKFRVIVSDGTYTPETVKGIVKVLIVLIDFSGAITHYIA 114
 QY 799 ALKAKKSPKGTI 811
 DB 115 SLLMKGLARGDI 127

RESULT 30 Q9V0C8 PRELIMINARY; PRT: 286 AA.
 ID Q9V0C8;
 AC Q9V0C8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE HYPOTHETICAL 31.4 KDA PROTEIN.
 GN PAB0578.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 NCBI_TaxID=29292;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;
 RA Heilig R.;
 RL "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ248285; CAB49776.1;
 DR HSSP: 045560; 1BWE.
 DR InterPro: IPR000707;
 DR InterPro: IPR001450;
 DR Pfam: PF00337; fer4; 2.
 DR Pfam: PF00991; para; 1.
 DR ProSite: PS00148; 4FR4S_FERREDOXIN; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 286 AA; 31430 MW; 54375F278B46DAFC CRC64;

Query Match 0.6%; Score 68; DB 1; Length 286;
 Best Local Similarity 27.3%; Pred. No. 21;
 Matches 21; Conservative 9; Mismatches 47; Indels 0; Gaps 0;
 QY 2049 IAGE-SVAMADUSLWKPINYQIIHKTRDSSEKVRFAALITVLALAKLKERYIVLLPSIP 2108
 DB 33 LADLDVEAPNDHLLGLVGLQNERFVHQFMKFNVAKCIKCKKCAFCVCEHAIIVLKGTIP 92
 QY 2109 LAFLEMEDECEVEHQ 2125
 DB 93 FLMPITCSGCRACRIVC 109

RESULT 31 Q9YVP8 PRELIMINARY; PRT: 409 AA.
 ID Q9YVP8;
 AC Q9YVP8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ORF MSV194 ALI MOTIF GENE FAMILY PROTEIN.
 GN MSV194.
 OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 NCBI_TaxID=83191;
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RA MEDLINE=99102512; PubMed=9847359;
 RA AF063866; Tulman E.P., Tu Z., Oms W., Kotish G.F., Rock D.L.;
 RL "The genome of Melanoplus sanguinipes entomopoxvirus."
 RL J. Virol. 73:533-552(1999).
 DR InterPro: IPR003497;
 DR Pfam: PF02498; BRO; 1.
 SQ SEQUENCE 409 AA; 48676 MW; A062DEF999B47D57 CRC64;

DR HSSP: P11746; IMNM.
DR Mendel: 32687; Mado: MADS; 42687.
DR InterPro: IPR002100; -
DR InterPro: IPR002487; -
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADS DOMAIN.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR SMART: SM00432; MADS; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 246 AA; 28278 MW; 641F35E21C887FA1 CF64;

Query Match 0.64; Score 67; DB 10; Length 246;
Best local similarity 18.94; Pred. No. 24;
Matches 18; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1819 PVLLPAIKTYQIEKNNKNNHMPFMSILOEHGIXMKKFEITSHQSQTAFPLEALDPR 1878
Db 84 PAKELSSYREYMKLGKGYESLQPTNPLIGDLPINLTKELFQLEGLSKQVRSTK 143

QY 1879 AQHSENDERVGKTENCIIDLCLVAMVVKLSEVIFR 1913
Db 144 TOYMLDQLSLQNKQKELLLEANKDLTKMLDEISSR 178

RESULT 41
ID Q9SHA6 PRELIMINARY; PRT: 246 AA.
AC Q9SHA6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MADS BOX PROTEIN.
DE MADS BOX PROTEIN.
GN MADS BOX PROTEIN.
OS MADS BOX PROTEIN.
OC Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; Eucosids I;
OC Eucosids; Rosaceae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. GRANNY SMITH;
RA YAO J., Dong Y., Kvarnheden A., Morris B.,
RA "Seven apple MADS-box genes are expressed in different parts of
RA fruit";
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL: AJ001681; CAA04319.1;
DR HSSP: P11746; IMNM.
DR InterPro: IPR000740; -
DR InterPro: IPR002100; -
DR InterPro: IPR002487; -
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADS DOMAIN.
DR PROSITE: PS002673; -1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR SMART: SM00432; MADS; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 246 AA; 28260 MW; 761F23E8B87FA2 CF64;

Query Match 0.64; Score 67; DB 10; Length 246;
Best local similarity 18.94; Pred. No. 24;
Matches 18; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1819 PVLLPAIKTYQIEKNNKNNHMPFMSILOEHGIXMKKFEITSHQSQTAFPLEALDPR 1878
Db 84 PAKELSSYREYMKLGKGYESLQPTNPLIGDLPINLTKELFQLEGLSKQVRSTK 143

QY 1879 AQHSENDERVGKTENCIIDLCLVAMVVKLSEVIFR 1913
Db 144 TOYMLDQLSLQNKQKELLLEANKDLTKMLDEISSR 178

RESULT 42
ID Q9FLV6 PRELIMINARY; PRT: 262 AA.
AC Q9FLV6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MADS BOX PROTEIN AGL2.
GN FL1PR 180
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; Eucosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneke T., Kato T., Asamizu F., Kotani H.,
RA Tabata S., Mewes H.W., Ruid S., Lemcke K., Meyer K.F.X.,
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RA EMBL: AL391144; CAC01779.1; -
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL: AL391144; CAC01779.1; -
DR InterPro: IPR002100; -
DR InterPro: IPR002487; -
DR Pfam: PF00319; SRF-TF; 1
DR Pfam: PF01486; K-box; 1
DR PRINTS: PR00404; MADS DOMAIN.
DR PROSITE: PS00350; MADS_BOX_1; 1
DR PROSITE: PS00066; MADS_BOX_2; 1
DR SMART: SM00432; MADS; 1
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 262 AA; 29914 MW; 6090357E800000 CF64;

Query Match 0.64; Score 67; DB 10; Length 262;
Best local similarity 18.14; Pred. No. 25;
Matches 15; Conservative 25; Mismatches 43; Indels 0; Gaps 0;

QY 1828 KTYKQIEKNNKNNHMPFMSILOEHGIXMKKFEITSHQSQTAFPLEALDPR 1887
Db 93 PEYKIKQRYENLQPCQPNLLCFNLPINLSKPIQLIEPQIDNSIKQVRSTKTYMLDLS 152

QY 1888 EVGKTENCIIDLCLVAMVVKLSEV 1910
Db 153 DLONKEQMLLETNRALAMKLDMM 175

RESULT 43
ID Q9FLV7 PRELIMINARY; PRT: 349 AA.
AC Q9FLV7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MZFL8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; Eucosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-COLUMBIA;

RX NCR_12432-3077;
 RP [1]
 RQ SEQUENCE FROM N.A.
 RR MEDLINE:97303241; PubMed:9159184;
 RS Wakasugi T., Naito T., Kapoor M., Saito M., Ito M., Ito S., and Ito
 SA Tsukaguchi J., Naito T., Kapoor M., Saito M., Ito S., and Ito
 SC Yamamura A., Yoshinaka K., Shikura M.,
 SD "Complete nucleotide sequence of the chloroplast genome from the green

100

Query Match	0.6%	Score 66	DB 5	Length 2470
Best Local Similarity	34.3%	Pred. No. 4,4e+02		
Matches 12	Conservative 13	Mismatches 10	Indels 0	Gaps
Q7	2070	LLKTPRSFVFPFAALITVIAFKFKENYVILP	2104	
DE	1123	LXPVLDAPFPIPPQAMTTPSTAKQIGKRYIVFVP	1167	
RESULT 62				
Q91908	PRELIMINARY	PRT: 2693 AA.		
ID	Q91908			
AC	Q91908			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
FC	SEQUENCE FROM N.A.			
RP	TISSUE-OVARY;			
RX	MEDLINE-93258819; PubMed-8397895;			
PA	Kume S., Mito A., Aruga J., Nakagawa T., Michikawa T., Furuichi T.,			
PA	Nakade S., Okano H., Mikoshiba K.;			
PT	"The Xenopus IP3 receptor: structure, function, and localization in			
PT	oocytes and eggs";			
RL	Cell 73:555-570(1993).			
DR	EMBL; D14400; BAA03304.1; -			
DR	InterPro: IPR000493; -			
DR	InterPro: IPR000699; -			

```

Query Match      0.68;   Score 66;   DB 5;   Length 2470;
Best Local Similarity 34.3%;   Pred. No. 4.4e+02;
Matches 12;   Conservative 13;   Mismatches 10;   Indels 0;   Gaps 0;

1 2070 LKLTPISSPKVFPFAALITVIATAPAKIKENYIVILP 2104
      11: 11:1 11: 11: 11:1 11: 11: 11:
2 1123 LPEVLDAPEPTIQDAMTTPRSIAKQIGKKYIVFVP 1167

RESULT 62
091908      PRELIMINARY;   PRT: 2693 AA.
091908;
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
01-MAR-2001 (TREMBlrel. 16, Last annotation update)
INSGIT01.1.4.5-TRIPHOSPHATE RECEPTOR.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Eupleuromorpha;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipodae; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
111
SEQUENCE FROM N.A.
TISSUE=OVARY;
MEDLINE=93258819; PubMed=8387895;
Kume S., Moto A., Aruga J., Nakagawa T., Furuichi T.,
Nakado S., Okano H., Mikoshiba K.;
"The Xenopus IP3 receptor: structure, function, and localization in
oocytes and eggs";
Cell 73:555-570(1993).
EMBL: D14400; BAA03304.1; -.
InterPro: IPR000493; -.
InterPro: IPR000699;

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RESULT 67					
91HN5					
ID	Q91HN5	PRELIMINARY:	PRT:	302 AA.	
AC	Q91HN5:				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	CAPSID PROTEIN VP1 (FRAGMENT).				
OS	Human poliovirus 1.				
CC	VIRUSES; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;				
OC	Enterovirus.				
OX	NCBI_TaxID=12080;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
PC	STRAIN=5937RUS94;				
BX	MEDLINE=203466204; PubMed=10906191;				
PA	Gavrillio G V., Cherkasova F A., Ilyskaya G Y., Kew O M., Anol V J.;				
FT	"Evolution of circulating wild poliovirus and of vaccine derived				
FT	poliovirus in an immunodeficient patient: a unifying model."				
PL	J. Virol. 74:7381-7390(2000)				
PR	EMRL AF333120; AAF35024.1; -				
DR	InterPro: IPRO01676; -				
DE	Pfam: PF000074; rhv; 1				
FT	NON_TER 1				
FT	NON_TER 302 302				
SEQ	SEQUENCE 302 AA: 33372 MW: AARFA079RRG66E1C CRC64;				
 Query Match 0 69: Score 65; DB 14; Length 302;					
Res: Local similarity 21 08: Prod No. 54;					
Matches 1/: Conservative 16; Mismatches 48; Indels 0; Gaps 0;					
Q3	481 TGLHSLNRLLALVELEAMHLRFETPTSECVVFETTFAV;APFCDRIUUVVISAISA 540				
DB	13: :				
OY	45 TAVETATNVVPSDVTQTTRIVIOHRSSSVESFEARGACVTIMSDNSDPTTSKRL 104				
DB	13: :				
OY	541 FEIPIKRHFSEKVITISNLINLP 561				
DB	13: :				
OY	105 ESWVKITYKTVDGIERKLEFP 125				
DB	13: :				
 RESULT 68					
Q9KG61					
ID	Q9KG61	PRELIMINARY:	PRT:	433 AA.	
AC	Q9KG61:				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	METHYL-ACCEPTING CHEMOTAXIS PROTEIN.				
OS	MCFA.				
GN	Bacillus halodurans				
OC	Bacteria; Firmicutes; Bacillus/clostridium group;				
OC	Bacillus/Staphylococcus group; Bacillus.				
OX	NCBI_TaxID=86665;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
PC	STRAIN=C-125 / JCM 9153;				
RP	Takami H., Nakasone K., Takaki Y.;				
RL	Submitted (MAP-Year) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: AP001519; BAB07487.1; -				
DP	InterPro: IPRO00127; -				
DE	Infernal: IPRO00658; -				

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DR SMART; SM00304; HAMP; 1.
SO SEQUENCE 433 AA; 46877 MW; F0D18C4E56A9E9FB CRC64;

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Query Match	C.68	Score	65	DB	2	Length	433
Best Local Similarity	27.38	Pred. No.	82				
Matches	15	Conservative	15	Mismatches	25	Indels	0
						Gaps	0

1980-1981, 1982-1983, 1984-1985, 1986-1987, 1988-1989, 1990-1991, 1992-1993, 1994-1995, 1996-1997, 1998-1999, 2000-2001, 2002-2003, 2004-2005, 2006-2007, 2008-2009, 2010-2011, 2012-2013, 2014-2015, 2016-2017, 2018-2019, 2020-2021, 2022-2023, 2024-2025, 2026-2027, 2028-2029, 2030-2031, 2032-2033, 2034-2035, 2036-2037, 2038-2039, 2040-2041, 2042-2043, 2044-2045, 2046-2047, 2048-2049, 2050-2051, 2052-2053, 2054-2055, 2056-2057, 2058-2059, 2060-2061, 2062-2063, 2064-2065, 2066-2067, 2068-2069, 2070-2071, 2072-2073, 2074-2075, 2076-2077, 2078-2079, 2080-2081, 2082-2083, 2084-2085, 2086-2087, 2088-2089, 2090-2091, 2092-2093, 2094-2095, 2096-2097, 2098-2099, 2100-2101, 2102-2103, 2104-2105, 2106-2107, 2108-2109, 2110-2111, 2112-2113, 2114-2115, 2116-2117, 2118-2119, 2120-2121, 2122-2123, 2124-2125, 2126-2127, 2128-2129, 2130-2131, 2132-2133, 2134-2135, 2136-2137, 2138-2139, 2140-2141, 2142-2143, 2144-2145, 2146-2147, 2148-2149, 2150-2151, 2152-2153, 2154-2155, 2156-2157, 2158-2159, 2160-2161, 2162-2163, 2164-2165, 2166-2167, 2168-2169, 2170-2171, 2172-2173, 2174-2175, 2176-2177, 2178-2179, 2180-2181, 2182-2183, 2184-2185, 2186-2187, 2188-2189, 2190-2191, 2192-2193, 2194-2195, 2196-2197, 2198-2199, 2200-2201, 2202-2203, 2204-2205, 2206-2207, 2208-2209, 2210-2211, 2212-2213, 2214-2215, 2216-2217, 2218-2219, 2220-2221, 2222-2223, 2224-2225, 2226-2227, 2228-2229, 2230-2231, 2232-2233, 2234-2235, 2236-2237, 2238-2239, 2240-2241, 2242-2243, 2244-2245, 2246-2247, 2248-2249, 2250-2251, 2252-2253, 2254-2255, 2256-2257, 2258-2259, 2260-2261, 2262-2263, 2264-2265, 2266-2267, 2268-2269, 2270-2271, 2272-2273, 2274-2275, 2276-2277, 2278-2279, 2280-2281, 2282-2283, 2284-2285, 2286-2287, 2288-2289, 2290-2291, 2292-2293, 2294-2295, 2296-2297, 2298-2299, 2300-2301, 2302-2303, 2304-2305, 2306-2307, 2308-2309, 2310-2311, 2312-2313, 2314-2315, 2316-2317, 2318-2319, 2320-2321, 2322-2323, 2324-2325, 2326-2327, 2328-2329, 2330-2331, 2332-2333, 2334-2335, 2336-2337, 2338-2339, 2340-2341, 2342-2343, 2344-2345, 2346-2347, 2348-2349, 2350-2351, 2352-2353, 2354-2355, 2356-2357, 2358-2359, 2360-2361, 2362-2363, 2364-2365, 2366-2367, 2368-2369, 2370-2371, 2372-2373, 2374-2375, 2376-2377, 2378-2379, 2380-2381, 2382-2383, 2384-2385, 2386-2387, 2388-2389, 2390-2391, 2392-2393, 2394-2395, 2396-2397, 2398-2399, 2400-2401, 2402-2403, 2404-2405, 2406-2407, 2408-2409, 2410-2411, 2412-2413, 2414-2415, 2416-2417, 2418-2419, 2420-2421, 2422-2423, 2424-2425, 2426-2427, 2428-2429, 2430-2431, 2432-2433, 2434-2435, 2436-2437, 2438-2439, 2440-2441, 2442-2443, 2444-2445, 2446-2447, 2448-2449, 2450-2451, 2452-2453, 2454-2455, 2456-2457, 2458-2459, 2460-2461, 2462-2463, 2464-2465, 2466-2467, 2468-2469, 2470-2471, 2472-2473, 2474-2475, 2476-2477, 2478-2479, 2480-2481, 2482-2483, 2484-2485, 2486-2487, 2488-2489, 2490-2491, 2492-2493, 2494-2495, 2496-2497, 2498-2499, 2500-2501, 2502-2503, 2504-2505, 2506-2507, 2508-2509, 2510-2511, 2512-2513, 2514-2515, 2516-2517, 2518-2519, 2520-2521, 2522-2523, 2524-2525, 2526-2527, 2528-2529, 2530-2531, 2532-2533, 2534-2535, 2536-2537, 2538-2539, 2540-2541, 2542-2543, 2544-2545, 2546-2547, 2548-2549, 2550-2551, 2552-2553, 2554-2555, 2556-2557, 2558-2559, 2560-2561, 2562-2563, 2564-2565, 2566-2567, 2568-2569, 2570-2571, 2572-2573, 2574-2575, 2576-2577, 2578-2579, 2580-2581, 2582-2583, 2584-2585, 2586-2587, 2588-2589, 2590-2591, 2592-2593, 2594-2595, 2596-2597, 2598-2599, 2600-2601, 2602-2603, 2604-2605, 2606-2607, 2608-2609, 2610-2611, 2612-2613, 2614-2615, 2616-2617, 2618-2619, 2620-2621, 2622-2623, 2624-2625, 2626-2627, 2628-2629, 2630-2631, 2632-2633, 2634-2635, 2636-2637, 2638-2639, 2640-2641, 2642-2643, 2644-2645, 2646-2647, 2648-2649, 2650-2651, 2652-2653, 2654-2655, 2656-2657, 2658-2659, 2660-2661, 2662-2663, 2664-2665, 2666-2667, 2668-2669, 2670-2671, 2672-2673, 2674-2675, 2676-2677, 2678-2679, 2680-2681, 2682-2683, 2684-2685, 2686-2687, 2688-2689, 2690-2691, 2692-2693, 2694-2695, 2696-2697, 2698-2699, 2700-2701, 2702-2703, 2704-2705, 2706-2707, 2708-2709, 2710-2711, 2712-2713, 2714-2715, 2716-2717, 2718-2719, 2720-2721, 2722-2723, 27

Journal of Management Inquiry 22(4) 399-414

May 1991

May 1991

in genetic groups. 7-9 and comparison with those in the other eight genetic groups. 7-9

J. Gen. Virol. 79:1847-1857(1998)

1- SEQUENCES: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NS1 IS CONTAINED WITHIN THE GENOME POLYPROTEIN E1: ENVELOPE GLYCOPROTEIN E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY SIMILARITY).

1- SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1 FAMILY.

1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.

1- SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.

EMBL: D84262; BAA32664.1; -

HSSD: P27958; 1A1V.

InterPro: IP000745; -

InterPro: IP0001410; -

InterPro: IP0001490; -

InterPro: IP0002166; -

InterPro: IP0002518; -

InterPro: IP0002519; -

InterPro: IP0002521; -

InterPro: IP0002522; -

InterPro: IP0002531; -

InterPro: IP0002888; -

InterPro: IP0003006; -

PFam: PF00998; HCV_RDRP; 1.

PFam: PF01001; HCV_NS4b; 1.

PFam: PF01306; HCV_NS4a; 1.

PFam: PF01506; HCV_NS5a; 1.

PFam: PF01538; HCV_NS2; 1.

PFam: PF01539; HCV_env; 1.

PFam: PF01542; HCV_core; 1.

PFam: PF01543; HCV_capsid; 1.

PFam: PF01560; HCV_NS1; 1.

ProDom: PD186062; -; 1.

PROSITE: PS00240; G_MHC; UNKN/WH 1.

SMART: SM00487; DEXDC; 1.

Coat protein, Envelope protein, Glycoprotein, Nonstructural protein, Polyprotein, RNA-directed RNA polymerase, Transmembrane.

SEQUENCE 3019 AA: 32632 MW: 826700070 Da 310 CRC64:

Query Match 0.6%; Score 65; DB 14; Length 3019;

Best Local Similarity 42.9%; Pred. No. 7; 4e+02;

Matches 12; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1822 LEPALKKTYGTFWNRKHHMGPPMSILQ 1849

DB 1751 LKPAIHSTWPKVEEFWRKHHMNFVSGIQ 1778

1 111 1 111 1 11 11 11 11

RESULT 79

Q9NMT6 PRELIMINARY: PRT: 53 AA.

AC Q9NMT6 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE PROBABLE CODED FOR BY C ELEGANS CDNA YK38H3.5 (FRAGMENT)

GN LM26.06.

OS Leishmania major.

OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID:5664;

PN 111

PP SEQUENCE FROM N.A.

RC STRAIN-FRIEDLIN;

RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;

RE Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.

RT EMBL: AL160493; CAB97624.1; -

FT NDR_TER 53 53

SQ SEQUENCE 53 AA: 6315 MW: 1E34B6A5678549D2 CRC64:

Query Match 0.6%; Score 64; DB 5; Length 53;

Best Local Similarity 36.6%; Pred. No. 10;

Matches 15; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 78 ERSVGTAVNKOLDNISLFLHLSPYFLKPAQKGLWLI 118

DB 13 ERSMLTTTSTLRVRLEQFLTLPHLFLTAQQVFEPLV 53

111 1 1 1 1 111 1 11 111

RESULT 80

Q9LV88 PRELIMINARY: PRT: 109 AA.

AC Q9LV88;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MXK3.

OS Arabidopsis thaliana (Mouse-ear cress);

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Eudicotyledons; Core eudicots; Fossids; eudicots II;

OC Brassicaceae; Brassicaceae; Arabidopsids.

OX NCBI_TaxID:3702;

PN 111

PP SEQUENCE FROM N.A.

RC STRAIN-COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,

RA Tabata S.;

RT Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones.;

RL DNA Res. 7:31-63(2000).

DR EMBL: AB019236; BAA97301.1; -

SQ SEQUENCE 109 AA: 12343 MW: 63C5E26BC71B42E CRC64:

Query Match 0.8%; Score 64; DB 10; Length 109;

Best Local Similarity 37.5%; Pred. No. 23;

Matches 15; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1456 VQBQIQSLMNIQVLLKPEKEELIFAVSFHFSQEE 1495

DB 18 VOFLDQALIAVLCIGLCCPAKKTAPSPVTFNQPEQEE 57

1 111 1 11 1 1 1 1 11 111 111

RESULT 81

Q9NZ23 PRELIMINARY: PRT: 219 AA.

AC Q9NZ23;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE HSPC177.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

PN 111

PP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;

RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,

RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;

RT "Human full length cDNA cloned from cd34+ stem cells.;"

BL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF161525; AAF29140.1; -

SQ SEQUENCE 219 AA: 24571 MW: C9969FF64FD7E126 CRC64:

Query Match 0.6%; Score 64; DB 4; Length 219;

Best Local Similarity 31.1%; Pred. No. 51;

Matches 14; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Query	Match	Score	DB	Length	878
Query Match	0.6%	Score 64	DB 14	Length 878	
Best local Similarity	17.8%	Prod No. 5002			
Matches	23	Conservative	26	Mismatches	80
				Indels	0
				Gaps	0
433	ESKYPRTDVLVFEHFKETADLKQELFHQFVSLSTSGGKYOFADSDTSLMSLNHPLA	492			
573	QSALPQGLLELSVAQAGALITSLPQQDLSLPTASGPAHSKEVPALTAVETGATNPLV	632			
493	PVRLAMNHLLKIMKTSKEGVDSFTKEAVLAPLGDNDIDVLSAISAFEIPIKEHFSSEV	552			
633	PSDIVQPHVIQRPSPSESTIESFFAPGAVAIIVQDNEQPTTRACKLFAIKWLIYKDTV	692			
553	TISNLLNLF 561				
693	QLRKKLEFF 701				
Query Match	0.6%	Score 64	DB 14	Length 878	
Best local Similarity	17.8%	Prod No. 5002			
Matches	23	Conservative	26	Mismatches	80
				Indels	0
				Gaps	0
433	ESKYPRTDVLVFEHFKETADLKQELFHQFVSLSTSGGKYOFADSDTSLMSLNHPLA	492			
573	QSALPQGLLELSVAQAGALITSLPQQDLSLPTASGPAHSKEVPALTAVETGATNPLV	632			
493	PVRLAMNHLLKIMKTSKEGVDSFTKEAVLAPLGDNDIDVLSAISAFEIPIKEHFSSEV	552			
633	PSDIVQPHVIQRPSPSESTIESFFAPGAVAIIVQDNEQPTTRACKLFAIKWLIYKDTV	692			
553	TISNLLNLF 561				
693	QLRKKLEFF 701				

Query Match 0.68; Score 64; DB 5; Length 1154;
 Best Local Similarity 29.48; Ref. No. 540-02;
 Matches 29; Conserved 10; Mismatches 48; Indels 0; Gaps 0;
 QY 360 NNDRITASIIFFEYVTSYSSQPEMISNKVSIINFGELDEITIFPSKYDPTIDVIVFFHLK 449
 DB 1081 NNAVHYMKIKFVKTIFISJIMENISENVIPEMFQETISVFIQIQEQRKDFYLKLIVE 1140
 QY 450 ELADLKQ 457
 DB 1141 YVAUMFQ 1148
 RESULT 97
 QYVW49 PRELIMINARY PRI: 1779 AA.
 AC QYVW49;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE CG8334 PROTEIN (FRAGMENT).
 GN CG8334.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CX MBL_TaxID 7227;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN: BERKELEY.
 MEDLINE 20196006; PubMed-1073 142;
 KA Adams M.D., Gehringer S.E., Holt R.A., Evans C.A., Gagey J.L.,
 KA Amalalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 KA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 KA Guiton K.A., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 KA Branton K.C., Rogers Y.H., Blazek R.G., Champ M., Pfeiffer W.J.,
 KA Wang K., Pezlo C., Rostor E., Walt G., Nelson C.K., Miklos G.L.G.,
 KA Abell J.P., Aylward A., An H.J., Andrews P., Bickel P., Bickel P.,
 KA Ballou R.M., Bass A., Baxendale J., Bayraktarolu L., Beasley E.M.,
 KA Beeson K.V., Benos P.V., Berman R.P., Blahut P., Bolshakov S.,
 KA Burkitt D., Burcham D.A., Butler H., Cadieu E., Center A., Chandra L.,
 KA Chert J.M., Chiswick S., Clarke C., Daye P., Davies P.,
 KA de Bablos B., DeChet A., Ben Z., Mays A., Jew L., Jett S.M.,
 KA Dodson K., Doup L.E., Downes M., Duncan-Kocha S., Duncker B., Dunn P.,
 KA Durbin C., Eganli A., Gera N.S., Gelbart W.M., Glasser K.,
 KA Glodex A., Goff J., Goff J., Gu Z., Guan P., Harris M.,
 KA Harris N.L., Harvey D., Heimar T.J., Hernandez J.F., Hock J.,
 KA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibequm C.,
 KA Jalali M., Kalush F., Karpen C.H., Ke Z., Kennison J.A., Ketchum R.A.,
 KA Kimmel B.E., Kralj T., Kralj T., Kralj T., Kralj T., Kralj T.,
 KA Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
 KA Liu X., Mattel B., McIntosh T.F., McLeod M.F., McPherson D.,
 KA Merklov G., Milshina N.V., Murphy B., Morris J., Moshiri A.,
 KA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D., Nelson D.,
 KA M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y.,
 KA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 KA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 KA Shue R.C., Shih-Klamos L., Simpson M., Skopets M.P., Smith T.,
 KA Spier R., Spradling A.C., Stapleton M., Strong R., Sun E.,
 KA Svirskas R., Teator C., Turner K., Ventor E., Wand A.H., Wand X.,
 KA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 KA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 KA Ye J., Ye R., Yeh F., Yeh F., Yeh F., Yeh F., Yeh F., Yeh F.,
 KA Zhou X.H., Zhou F.N., Zhou W., Zhou X., Zhou X., Zhou X., Zhou X.,
 KA Gibbs R.A., Myers E.W., Rubin G.M., Ventor J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 CL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DB EMBL: AF003515; AAF49100.2;
 DB HSP: P02588; IINX.
 DB FlyBase: FBgn0046913; CG8334.

Query Match 0.68; Score 64; DB 5; Length 1154;
 Best Local Similarity 29.48; Ref. No. 540-02;
 Matches 29; Conserved 10; Mismatches 48; Indels 0; Gaps 0;
 QY 360 NNDRITASIIFFEYVTSYSSQPEMISNKVSIINFGELDEITIFPSKYDPTIDVIVFFHLK 449
 DB 1081 NNAVHYMKIKFVKTIFISJIMENISENVIPEMFQETISVFIQIQEQRKDFYLKLIVE 1140
 QY 450 ELADLKQ 457
 DB 1141 YVAUMFQ 1148
 RESULT 97
 QYVW49 PRELIMINARY PRI: 1779 AA.
 AC QYVW49;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE CG8334 PROTEIN (FRAGMENT).
 GN CG8334.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CX MBL_TaxID 7227;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN: BERKELEY.
 MEDLINE 20196006; PubMed-1073 142;
 KA Adams M.D., Gehringer S.E., Holt R.A., Evans C.A., Gagey J.L.,
 KA Amalalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 KA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 KA Guiton K.A., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 KA Branton K.C., Rogers Y.H., Blazek R.G., Champ M., Pfeiffer W.J.,
 KA Wang K., Pezlo C., Rostor E., Walt G., Nelson C.K., Miklos G.L.G.,
 KA Abell J.P., Aylward A., An H.J., Andrews P., Bickel P., Bickel P.,
 KA Ballou R.M., Bass A., Baxendale J., Bayraktarolu L., Beasley E.M.,
 KA Beeson K.V., Benos P.V., Berman R.P., Blahut P., Bolshakov S.,
 KA Burkitt D., Burcham D.A., Butler H., Cadieu E., Center A., Chandra L.,
 KA Chert J.M., Chiswick S., Clarke C., Daye P., Davies P.,
 KA de Bablos B., DeChet A., Ben Z., Mays A., Jew L., Jett S.M.,
 KA Dodson K., Doup L.E., Downes M., Duncan-Kocha S., Duncker B., Dunn P.,
 KA Durbin C., Eganli A., Gera N.S., Gelbart W.M., Glasser K.,
 KA Glodex A., Goff J., Goff J., Gu Z., Guan P., Harris M.,
 KA Harris N.L., Harvey D., Heimar T.J., Hernandez J.F., Hock J.,
 KA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibequm C.,
 KA Jalali M., Kalush F., Karpen C.H., Ke Z., Kennison J.A., Ketchum R.A.,
 KA Kimmel B.E., Kralj T., Kralj T., Kralj T., Kralj T., Kralj T.,
 KA Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
 KA Liu X., Mattel B., McIntosh T.F., McLeod M.F., McPherson D.,
 KA Merklov G., Milshina N.V., Murphy B., Morris J., Moshiri A.,
 KA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D., Nelson D.,
 KA M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y., M. Y.,
 KA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 KA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 KA Shue R.C., Shih-Klamos L., Simpson M., Skopets M.P., Smith T.,
 KA Spier R., Spradling A.C., Stapleton M., Strong R., Sun E.,
 KA Svirskas R., Teator C., Turner K., Ventor E., Wand A.H., Wand X.,
 KA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 KA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 KA Ye J., Ye R., Yeh F., Yeh F., Yeh F., Yeh F., Yeh F., Yeh F.,
 KA Zhou X.H., Zhou F.N., Zhou W., Zhou X., Zhou X., Zhou X., Zhou X.,
 KA Gibbs R.A., Myers E.W., Rubin G.M., Ventor J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 CL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DB EMBL: AF003515; AAF49100.2;
 DB HSP: P02588; IINX.
 DB FlyBase: FBgn0046913; CG8334.

[illegible]

RA Ohta N., Suzuki K., Hattori Y., Uraji M., Kato A., Yoshida K.,
 RT "Genomic structure of pTI-SAKURA (111). Characteristics of T-DNA.",
 RL Nucleic Acids Symp. Ser. 40:185-186(1998).
 RN [5]
 RC STRAIN MAPF301001;
 RA Uraji M., Suzuki K., Ohta N., Hattori Y., Kato A., Yoshida K.,
 RT "Genomic structure of pTI-SAKURA (11V). Characteristics of tra region.",
 RL Nucleic Acids Symp. Ser. 39:187-188(1998).
 RN [6]
 RC STRAIN MAPF301001;
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Kato A., Yoshida K.,
 RT "Genomic structure of pTI-SAKURA (V). Complete nucleotide sequence of
 plasmid pTI-SAKURA's vir region in *Agrobacterium tumefaciens*.",
 RL Nucleic Acids Symp. Ser. 39:265-266(1998).
 DR EMBL: AB016260; BAA87712.1;
 DR InterPro: IPR000479;
 DR PROSITE: PS00120; LIPASE_SBR; UNKNOWN_1.
 KW Plasmid.
 SQ SEQUENCE 458 AA; 48508 MW; DF18307751CF087B CRC64;

Query Match 0.6%; Score 63; DB 2; Length 358;
 Best Local Similarity 40.0%; Pred. No. 1.2e+02;
 Matches 14; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 372 GQYVRELEA:LFKISLERNHDLASLFFPPVVS 406
 ID 111 1111 11111 1111 1111
 DB 213 GKLGKLTASELPISLKNKSRLLASLIRGQHVA 247

RESULT 111
 Q9N3R0 PRELIMINARY; PRT; 366 AA.
 AC Q9N3R0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE MIRANDA (FRAGMENT).
 GN MIRANDA.
 OS Drosophila yakuba (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7245;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE: 20293933; PubMed:10923947;
 RA Begun D.J., Whitely P.,
 RT "Reduced X linked nucleotide polymorphism in *Drosophila simulans*.",
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5360-5365(2000).
 DR EMBL: AF255319; AAF66615.1;
 DR FlyBase: FBgn0041641; DyakXmiranda.
 FT NON_TER 1
 FT NON_TER 366 366
 FT SEQUENCE 366 AA; 42315 MW; 624E1EE301E3E2 CRC64.

Query Match 0.6%; Score 63; DB 5; Length 366;
 Best Local Similarity 46.7%; Pred. No. 3.2e+02;
 Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 QY 1176 TVQCFFPPCFMAGKRFSGVPSVQVYVYSYVQ 1205
 ID 111 1111 1111 1111
 DB 1 TECCGALPKVCCQVESDIESAVFERKSYWR 40

RESULT 112
 Q9K010 PRELIMINARY; PRT; 522 AA.
 ID Q9K010
 AC Q9K010;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE INVOLVED IN SPORE CORTEX SYNTHESIS.
 GN SPOVB.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN C-125 / JCM 9153;
 RA Takami H., Nakasono K., Takaki Y.;
 RL Submitted (MAP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF001511; BAR04952.1;
 DR InterPro: IPR002797;
 DR Pfam: PF01943; Polysacc synt; 1.
 SQ SEQUENCE 522 AA; 56157 MW; 29756518FF145AP CRC64;

Query Match 0.6%; Score 63; DB 2; Length 522;
 Best Local Similarity 22.9%; Pred. No. 1.8e+02;
 Matches 19; Conservative 19; Mismatches 46; Indels 0; Gaps 0;
 QY 170 CVDPLAGSLLHFCYKSLHMDLFISSVTSKVVFAHFGSSAQIKVLLAYAYAGVSAIV 229
 ID 111 111 111 111 111 111 111 111 111 111
 DB 146 GLGNKPTATYSQVIFQWVITPVVALLISAFPLIGVRYAAAGAMLSVVLGELASLLTVM 205

RESULT 113
 Q9T110 PRELIMINARY; PRT; 535 AA.
 AC Q9T110;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HEAD-TO-TAIL JOINING PROTEIN.
 GN Bacteriophage phiYe03-12.
 OS Bacteriophage phiYe03-12.
 OC Viruses; dsDNA viruses, no RNA stage; tailed phages; Podoviridae;
 OC T7-like phages.
 OX NCBI_TaxID=110457;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Pajunen M.L., Kiljunen S.J., Skurnik M.;
 RT "Complete genomic sequence of the lytic bacteriophage phi-ye03-12 of
 Yersinia enterocolitica serotype O:3.",
 RL Submitted (Nov. 1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AT253485; CARG3627.1;
 SQ SEQUENCE 535 AA; 58649 MW; 048688B0D64B2B80 CRC64;

Query Match 0.6%; Score 63; DB 9; Length 535;
 Best Local Similarity 25.9%; Pred. No. 1.9e+02;
 Matches 15; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
 QY 1551 LSTVGYISAVAGSMEFNALDELTVFWFALISKAYGLDKVNALLFTETTFIPVIRGLV 1608
 ID 111 111 111 111 111 111 111 111 111 111
 DB 318 LEAFISVAPINSVAGQTFQVTAFFIPYVASPEFTDITGVYSTISQPIQPIVRLVLL 405

RESULT 114
 O17044 PRELIMINARY; PRT; 699 AA.
 ID O17044
 AC O17044;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE BIG BRAIN (HIB).

OX	NCHL_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Almscough R.;

100

RN SEQUENCE FROM N.A.
 RC STRAIN CV, ZHANGHUA 8, TISSUE FLOWER,
 RA Gu L.J., Zhang Y., Liu M., Gu H., Chen Z.;
 RL Chin. Sci. Bull. 0:0-0(0).
 CC 1- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC 2- SIMILARITY TO THE RALS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 CC 3- SIMILARITY TO THE RALS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL: Y15008; CAA75241.1; .
 DR EMBL: Y1746; IMNR.
 DR MIMBL: 24250; GYSA; MAJ6; 21350.
 DR MIMBL: 24250; GYSA; MAJ6; 21350.
 DR InterPro: IPR002100; .
 DR InterPro: IPR002487; .
 DR Pfam: PF00319; SRP3E; 1.
 DR Pfam: PF01486; K-box; 1.
 DR PRINTS: PK03404; MADS_BOX_1; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00366; MADS_BOX_2; 1.
 DR SMART: SM00432; MADS; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SW SEQUENCE 249 AA; 28762 MW; 70921830ADA3330 CRC64;

Query Match 0.6%; Score 62; DB 10; Length 249;
 Best Local Similarity 21.8%; Pred. No. 1.1e+02;
 Matches 19; Conservative 20; Mismatches 48; Indels 0; Gaps 0;

QY 1223 LPALPTKTPYIFPMKSHNTPMCHHCHCHXKPKELTSLQVOLTAFPEALDFRACHS 1842
 DB 90 LEASRGYALKAFVRLTETLSELTETLSTETPTSTPKETGVYKIVPTPTPTPL 140
 QY 1883 ENLEIVGKTENGLDGLVAMVVKLSE 1409
 DB 150 VDGTELQKLEQWSEANPGLPKLEE 176

RESULT 145
 Q908V4 PRELIMINARY; PRT: 250 AA.
 AC Q908V4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE SEC-LIKE C (FRAGMENT).
 OS Eptatretus barretti (Inshore hagfish).
 CC Eukaryota; Metazoa; Chordata; Gracilata; Hyperotretii; Myxiniiformes;
 CC Myxiniidae; Eptatretinae; Eptatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE 20026339; PubMed 10552041;
 PA Suga H., Hoshiyama B., Kuraku S., Kato H., Kubokawa K., Miyata T.;
 RT "Protein tyrosine kinase CDNAs from amphioxus, hagfish, and lamprey;
 RT isoform duplications around the divergence of cyclostomes and
 RT gnathostomes."

J. Mol. Evol. 49:601-608(1999).
 EMBL: AB025548; BAA84738.1; .
 HSSP: P12931; IPMK.
 DR InterPro: IPR000719; .
 DR InterPro: IPR001245; .
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR SMART: SM00219; TYRK; 1.
 KW ATP-binding; Tyrosine-protein kinase.
 FT N-TER
 SW SEQUENCE 250 AA; 28437 MW; 65F66D2F1D0BAF0A CRC64;

Query Match 0.6%; Score 62; DB 13; Length 250;
 Best Local Similarity 27.9%; Pred. No. 1.1e+02;
 Matches 12; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1210 ILELIQHKKKLESPQIIVPILFNLISQCLPPEPQOCNMEYTK 1252
 DB 183 VLEEVGEYEMISTETETETELANAMCWFQCFETFTTFYLF 230
 RESULT 146
 Q9P156 PRELIMINARY; PRT: 266 AA.
 ID Q9P156
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE LY49J PROTEIN.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE 99299355; PubMed 10360927;
 RA McQueen K.L., Lohwasser S., Takai F., Major D.L.;
 FT "Taxi-scan analysis of new ly49 genes: most transcripts of ly49; 1-4
 FT the transmembrane domain."

EMBL: AF110492; AAF44052.1; .
 DR HSSP: P05451; LIT.
 DR InterPro: IPR001304; .
 DR Pfam: PF00059; lectin_3; 1.
 DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
 DR SMART: SM00034; CLECT; 1.
 SW SEQUENCE 266 AA; 31393 MW; EC7ED907968EEA60 CRC64;

Query Match 0.6%; Score 62; DB 11; Length 266;
 Best Local Similarity 25.0%; Pred. No. 1.1e+02;
 Matches 18; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

QY 665 IELIADNINLGDPSSMLKVEDLISGEESEFNKQKVTFTVILSVLSCSSLKETHPP 724
 DB 4 LEVYSTVNLHKSSGLKLVREUETQCTREAGNPGCSIYWGIVFALGILCFLLLVIVAV 63
 QY 725 FAHVFSLLQKK 736
 DB 64 IAKTFQYSQHR 75

RESULT 147
 Q9MBR9 PRELIMINARY; PRT: 267 AA.
 ID Q9MBR9
 AC Q9MBR9
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE ORF 20.
 OS Staphylococcus aureus prophage phIPW83.
 CC Viruses.
 OX NCBI_TaxID=129009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=P83;
 RA Zou B., Kaneko J., Narita S., Kamio Y.;
 RT "Complete nucleotide sequence and molecular characterization of
 RT prophage PV83pro carrying lukM-lukP-PV(P83) gene cluster in
 RT Staphylococcus aureus strain P83."

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P83;
 EX MEDLINE 98067870; PubMed 9404084.
 PA Kaneko J., Muramoto K., Kamio Y.;
 FT "Gene of lukP-PV-like component of panton-Valentine leukocidin in
 RT Staphylococcus aureus p83 is linked with lukM."


```

EMBL: AJ286081; CAB77542.1;
NON_TER      1
NT           348
SEQUENCE     348 AA; 38758 MW; 0362DB14E4AE10EA CPO64;

Query Match          0.6%; Score 62; DB 14; Length 348;
Best local Similarity 17.8%; Pred. No. 1,6e+02;
Matches 2; Conservative 27; Mismatches 79; Indels 0; Caps 0;

ay 433 ESKYPTDLDVWLEHHKEIADLKKQELFQFVSLSSTGGKYQFLAHSPTSILMLSLNHPLA 492
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ab 10 QSALPQGLIEDLISPVAGGALTSLIPRQQLSILPTRKASGFPAHSEKVEPAUTAVETGATNPLA 69

ay 493 PVELLANHLLKKMTFSFEVFSEFTFKFAVAIAHSGDNIDVVISALSARELFKEHFSSIV 552
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
db 70 PSDTVQTPHPVQSPSPSESTIESFFAFACVALIVIREQQTTEAQFLMMMPITYPTIV 129

ay 553 TISNLINLF 561
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
db 130 QIRPKLEEF 138

RESULT 152
ayXXVIB PRELIMINARY; PRT: 364 AA.
ayXVIB;
ayOT 01-NOV-1999 (TrEMBLrel. 12, Created)
ayOT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
ayOT 01-MAY-2000 (TrEMBLrel. 13, last annotation update)
ayDE I2265_3 PROTEIN.
aySN I2265_3.
aySN Caenorhabditis elegans.
ayDC Eukaryota; Metazoa; Nematoda; Chromadorea; Platyhelminthes;
ayDC Rhabdillidae; Poliderridae; Caenorhabditis.
ayDX NCBI_TaxID=4239;
ayRN [1]
ayRP SEQUENCE FROM N.A.
ayRA Smyr S.;
ayRL Submitted (JUL 1996) to the EMBL/GenBank/Fair databases.
ayRN [2]
ayRP SEQUENCE FROM N.A.
ayRX MEDLINE 94150718; PubMed 7906398;
ayRX Willson K., Alnscough R., Anderson K., Haynes C., Herks M., Coulson A.,
ayRA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
ayRA Craxton M., Dear S., De Zeeuw D., Durbin R., Favetto A., Fulton L.,
ayRA Gardner A., Green P., Hawkins T., Hillier L., Hjerpe M., Johnston L.,
ayRA Jones M., Kershaw J., Kirsten J., Laister R., Patterson R., Paterson L.,
ayRA Lightning J., Lloyd G., McMurry J., McQuibban R., O'Callaghan M.,
ayRA Parsons J., Percy G., Pitken L., Poopra A., Saunders D., Showkeen R.,
ayRA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
ayRA Thierry-Mieg J., Thomas K., Vaulin M., Vaughan F., Watkinson F.,
ayRA Watson A., Weinstock L., Wilkinson-Spoit J., Wohlman P.,
ayRT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
ayRT elegans."
ayRL Nature 358:32-38(1994).
ayDR EMBL: Z81127; CAB03388.1;
ayDR InterPro: IPROU1810;
ayDR Pfam: PF00646; F-box, 1.
aySO SEQUENCE 364 AA; 42740 MW; B61B0C9CCBC3D3F0 CPO64;

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Query Match	0.6%	Score 62	DB 5	Length 364;
Best Local Similarity	45.1%	Pred. No. 1.6e+02		
Matches 13	Conservative 7	Mismatches 17	Indels 0	Gaps 0;

QY	115	GISVNAEVRLELPPKAKLGIVACRFKKM ₂₈ K	1185
		: : : : : :	
bb	257	CAATGRRERFELPDLKTLITGLTKNAELVCPKO	293
		: : : : : :	

RESULTS 153
CONCLUSIONS 153

093601	PRELIMINARY;	PRT;	366 AA.
Q93601			
AC	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
DE	APOLIPOPROTEIN AIV.		
DE	APOLIIV.		
OS	Gallus gallus (Chicken).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neoquathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
OX	NCBI_TaxID=9031;		
RH	[1]		
RP	SEQUENCE FROM N.A.		
RP	MELLINE=98221191; PubMed=9553114;		
EX	Steinmetz A., Hermand M., Nimpi J., Aebersold R., Ducrot A.,		
PA	Weinberg P., Schneider W.J.;		
PA	"Expression and conservation of apolipoprotein AIV in an avian		
RT	species.";		
RT	J. Biol. Chem. 273:10543-10549(1998).		
RL	EMBL: Y16534; CAA76273.1; -.		
DR	InterPro: IPR000074; -		
DR	Plan: PF01442; Apolipoprotein; 1.		
DR	lipoprotein.		
KW	lipoprotein.		
SC	SEQUENCE 366 AA; 40852 MW; R47DB49F3ERD9ICE CRC64;		
QY	Query Match		
QY	Best Local Similarity 25.0%; Pred. No. 1.7e+02;		
QY	Matches 17; Conservative 16; Mismatches 35; Indels 0; Gaps 0;		
QY	1305 LLLGLGVAGIFPPKUKLHINSHITFMGANVMRIIDYTSQVINKVMVIFALQDSGD 1364		
DE	12 LAVACTEALVPEVQVATVLPVETFGSSAFFVDEGQAEETKQALHIGVNSASSEY 71		
QY	1365 STKVSRRV 1372		
QY	: : : :		
DB	72 AEEQLRRH 79		
RESULT 154			
Q9SE57	PRELIMINARY;	PRT;	381 AA.
Q9SE57			
AC	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000 (TREMBLrel. 16, Last annotation update)		
DE	CYTTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT1).		
DE	COX2.		
OS	Neonotonia whightii.		
OS	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eucosids 1;		
OC	Fabales; Fabaceae; Papilionoideae; Neonotonia.		
OX	NCBI_TaxID=103823;		
OX	NCBI_TaxID=103823;		
RH	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=20846642; PubMed=10570164;		
EX	Adams K.L., Somp K., Roessler P.G., Nugent J.M., Doyle J.L.,		
PA	Doyle J.L., Palmer T.D.;		
PA	"Intracellular gene transfer in action: Dual transcription and		
RT	multiple silencings of nuclear and mitochondrial cox2 genes in		
RT	legumes.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 96:13863-13868(1999).		
RL	1 FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY		
RL	CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-		
CC	3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2		
CC	TRANSFERS THE ELECTRONS FROM CYTOCHROM P C VIA ITS BINUCLEAR COPPER		
CC	A CENTER TO THE BINETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY		
CC	SIMILARITY).		
CC	-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2O) + 4		
CC	FERRICYTOCHROME C (BY SIMILARITY).		
CC	-1- COFACTOR: COPPER AND HEME GROUP (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; MITOCHONDRIAL		

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh K.-F., Zeng J.-S., Zhao M., Zhang C., Zhao Q., Zhong L.,
 RA Zhou X.-H., Zhou E.H., Zhou K.W., Zhou J.C., Zhou S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RI Science 287:2185-2195(2000).
 DR FMBL: AF003734; AAF55892.1;
 DR FlyBase: FB003866; CG6475.
 DR InterPro: IPR002213;
 DR Pfam: PF00201; UDRGT; 1.
 DR PROSITE: PS00375; UDRGT; 1.
 SQ SEQUENCE 441 AA; 50073 MW; AB74BA044714C0B2 CRC64;

Query Match 0.6%; Score 62; DB 5; Length 441;

Best Local Similarity 20.4%; Pred. No. 26+02;

Matches 11; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 474 TKEHLEADLTKLSKNNHGLASLHLYVSQGFHDEKVKSLRQFAP 427

DB 141 VISEMSTLFEVTEVFQHTSVLITTEMTITQEPWQGNWVQCHILP 194

RESULT 159

QVW759

AC QVW759

DT 01-NOV-1999 (TEMBLrel. 12, Created)

DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)

DE 94.6% IDENTICAL TO US GENE OF STRAIN U1102 OF HHV-6.

GN 65

OS Human herpesvirus 6.

OC Viruses, dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Roseolovirus.

OX NCBI_TaxID:10368;

KN [1]

SEQUENCE FROM N.A.

RP STRAIN-HSI

RA Isegaux Y., Makai T., Nakai K., Nakai M., Chan J., Mori Y.,

RA Saitawa T., Saitohara J., Kato T., Kozuka H., Yamanishi K.,

RT "A comparison of the complete DNA sequences between human herpesvirus

6, variant A and B."

RL J. Virol. 0:0-0(1999).

DR EMBL: AB021506; BAA78225.1; -

SQ SEQUENCE 443 AA; 51515 MW; 0D1F16807035191 CRC64;

Query Match 0.6%; Score 62; DB 14; Length 443;

Best Local Similarity 30.0%; Pred. No. 2,16+02;

Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1392 EHRPLPLVMTLGAKEFTWLLILLFFQYVTKTVLAAYGKDALLEADTEFWFVC 1451

DB 188 FHSRPLSLSTVTPDKKALFLTRVFVTFVFNLYAKVTHAELGYYDLEFEVGEKLC 247

RESULT 159

QVW759

AC QVW759

DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)

DE CG12960 PROTEIN.

GN CG12960.

OS *Drosophila melanogaster* (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; *Drosophila*.

OX NCBI_TaxID-7227;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN-BURKELEY;
 RC MFR1 INF-20196306, PubMed 10731132;
 PX Adams M.D., Celiniker S.E., Holt P.A., Evans C.A., Gocayne J.D.,
 RA Amaratides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George P.A., Lewis S.F., Ralston P., Zhang Q., Chen L.X.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chai L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blakes B.G., Champ M., Pfeiffer B.D.,
 RA Wan K.H., Dewis S., Holt P.A., Nelson C.P., Wilson G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Trankoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra L.,
 RA Chertif J.M., Cawley S., Dahlke C., Davenport I.R., Davies P.,
 RA de Patris R., Delcher A., Deng Z., Mays A.D., Dew L., Dietz S.M.,
 RA Dordick K., Doup E.E., Downes M., Duqu Rochas S., Dunkov B.C., Dunn P.,
 RA Durbin K., Eickholt J.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Finkler K., Fong A., Garg N.S., Gelbart W.M., Glasser K.,
 RA Foster A., Garg P., Corvelli T.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Heston D., Houston K.A., Howland T.J., Wei M.-H., Ikegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel R.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Y., Liang Y., Lin X.,
 RA Liu X., Mattei R., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mohanty C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L.,
 RA Nelson D.F., Nelson K.A., Nixon K., Nusskern D.P., Pachter J.M.,
 RA Palamara M., Pittman C.S., Pan S., Pollard T., Puri V., Reese M.G.,
 RA Peierl K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamus I., Simpson M., Skopski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Switzkes F., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh K.-F., Zeng J.-S., Zhao M., Zhang C., Zhao Q., Zhong L.,
 RA Zhou X.-H., Zhou E.H., Zhou K.W., Zhou J.C., Zhou S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RI Science 287:2185-2195(2000).
 DR FMBL: AF003734; AAF55892.1;
 DR FlyBase: FB003866; CG12960.
 SQ SEQUENCE 491 AA; 57573 MW; 8CB320ABBE95A0F5 CRC64;

Query Match 0.6%; Score 62; DB 5; Length 491;

Best Local Similarity 28.8%; Pred. No. 2,3e+02;

Matches 16; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 1900 LALQILNCLYKFLFDIQHPLSKERAAALMPLVLVDLENLGGGRKFKQVTKHL 2045

DB 203 LSTFVCLFSLVLIYVQLSWKNLTLANILLNDRKSLRGLLGSFPFPPNPKHL 258

RESULT 160

Q90407

ID Q90407

AC Q90407

DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)

DE RED-BIOLIMINSCENCE ELICITING LUCIFERASE.

OS *Phrixothrix hirtus*.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;

OC Elateriformia; Cantharidae; Phengodidae; Phrixothrix.

OX NCBI_TaxID-94779;

RN [1]

SEQUENCE FROM N.A.

PX MEDLINE: 94315203; PubMed: 10387072;

RA Reiner K., Komagata K., Sanders R.D.C., Schaefer F., Shen H.,
RA Shue B.C., Siden Kinos L., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong K., Sun E.,
RA Szelesky P., Turner C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,
RA Williams S.M., Woodard T., Worley K.F., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh K.-T., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhou X.H., Zhou F.M., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.G.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Brosophila melanogaster*,";
RL Science 287:2185-2195(2000).
DR EMBL: AF003515; AAF49097.1; -;
DR FlyBase: FBp003615; CG7757.
SQ SEQUENCE 598 AA; 67382 MW; DC5DADID4955FDEDE CRC64;

Query Match 0.6%; Score 62; Db 5; Length 598;
Best Local Similarity 35.4%; Pred. No. 2 9e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1160 SQPESVQVWGVGVWQVPTVITFLI:SHPPVPS 1223
Db 414 TQLETVDDASGKISIRQTAITNLIRPTQMKPP 347

RESULT 163
Q9KQF7 PRELIMINARY; PRT; 600 AA.
AC Q9KQF7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HYPOTHELICAL PROTEIN VC2041.
GN VC2041.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OC NCBI_TaxID=566;
RN [1]
RT "SEQUENCE FROM N.A."
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RE MEDLINE=20406833; PubMed=10952301;
RA Reddell J.F., Eisen J.A., Nelson W.C., Clayton P.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Emolaeva M.D., Vamathevan J., Bass S., Qin H., Braroi L., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.G., Colwell R.F., McEldowney T.L., Venter J.C.,
RA Fraser C.M.;
RA "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RI cholerae,";
RL Nature 406:477-483(2000).
DR EMBL: AE004278; AAF95189.1; -;
DR TIGR: VC2041; -;
SQ SEQUENCE 600 AA; 68371 MW; AFEF449F470794A CRC64;

Query Match 0.6%; Score 62; Db 2; Length 600;
Best Local Similarity 25.0%; Pred. No. 2 9e+02;
Matches 19; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

QY 1305 LLLCTVACITPDKVLNIMSFTHMCANVMPIDITYSFVINKTVKVV;PAGTQSHSD; 1364
Db 70 LLLVPLPFLTPSRLFLRLAVCTSLHGLVLLDTQAYQVILNHLRPVVWLLFSDETS 129

QY 1365 STFSRNVEIVKRI 1380
Db 130 SVSADLQHLFVVVLLI 145

RESULT 164
P72401 PRELIMINARY; PRT; 649 AA.
U72301
AC P72301;

DT 01-PRR-1997 (TrEMBLrel. 02, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PHOSPHOGLYCEROL TRANSFERASE.
GN CGB.
OS *Rhizobium meliloti* (*Sinorhizobium meliloti*).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phlobacteraceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RT "SEQUENCE FROM N.A."
RC STRAIN=1021.
RA Wang P., Ingram-Smith C., Hadley J.A., Miller K.J.;
RT "Cloning, sequencing, and characterization of the *cgmB* gene of
RT *Sinorhizobium meliloti* involved in cysteine beta-alanine biosynthesis,";
DR J. Bacteriol. 0:0-0(1999).
DR EMBL: U67998; AAR41531.2; -;
KW Transferase.
SQ SEQUENCE 649 AA; 71500 MW; CBAAC+GHP+PA588A CRC64;

Query Match 0.6%; Score 62; Db 2; Length 649;
Best Local Similarity 27.4%; Pred. No. 3 2e+02;
Matches 23; Conservative 14; Mismatches 47; Indels 0; Gaps 0;

QY 1566 ERNADKLIVKFWKALLSKAYDLDLKVNALLPTEFTFIVIKGLVGNFLFSVRRKALDLNN 1625
Db 141 EENLDLPLVAFEPFVHGH;EAVVSVLCHATFISFHHATGKFKVALDLRVIRIAGLRT 200

QY 1626 KLOQNSWKKTIIVTRFLKLVPLDL 1649
Db 201 MAIQGCHREKEFGVLFVRIADDFL 224

RESULT 165
O95364 PRELIMINARY; PRT; 651 AA.
AC O95364;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NON-RECEPTOR TYROSINE KINASE.
GN TNK1
OS *Homo sapiens* (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RT "SEQUENCE FROM N.A."
RA Hoeft G.L., Felschow D.M., Givin C.L.;
RC "Genomic structure and chromosomal mapping of the human non-receptor
RT tyrosine kinase gene, *Tnk1*,";
RL Submitted (01-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097738; AAC99412.1; -;
DR HSSP: PC6213; TIRK.
DR InterPro: IPR000719; -;
DR InterPro: IPR001245; -;
DR InterPro: IPR001452; -;
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00018; SH3; 1.
DR FEAT: PF00709; TYROSINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART: SM00326; SH3; 1.
KW ATP-Binding, Kinase, Receptor, Tyrosine-protein kinase.
SQ SEQUENCE 661 AA; 71326 MW; GA20P29221777DP CRC64;

Query Match 0.6%; Score 62; Db 4; Length 661;
Best Local Similarity 27.7%; Pred. No. 3 2e+02;
Matches 13; Conservative 13; Mismatches 21; Indels 0; Gaps 0;


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GN MIRA OR MIRANDA OR CG12244
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE=98065952; PubMed=9403694;
RA Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.Q.,
RA Matsuzaki F.;
RT "Miranda directs Prospero to a daughter cell during Drosophila
PT asymmetric divisions.";
RL Nature 390:625-629(1997);
DR EMBL: AB005661; BAA24111.1; -.
DR FlyBase: FBgn0021776; miranda.
SQ SEQUENCE 830 AA; 93171 MW; F7AD159AA58F178A CPG64;

Query Match 0.6%; Score 62; DB 5; Length 830;
Best Local Similarity 45.7%; Pred. No. 4.2e+02;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Q7 1176 TVGKPPKMKQKKSQLESVQVGGSYWQ 1205
Db 402 TEQQAVAKVQQVESDESAREKSYWR 431
|||||
|||||

RESULT 171
045116 PRELIMINARY; PRT; 830 AA.
AC 045116;
DT 01-JUN-1998 (TRENBLREL 06, Created)
DT 01-JUN-1998 (TRENBLREL 06, Last sequence update)
DT 01-MAR-2001 (TRENBLREL 16, Last annotation update)
DE MIRANDA.
GN MIRA OR MIRANDA OR CG12244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CANTON-S;
RX MEDLINE=97410310; PubMed=9267025;
RA Shen C.P., Jan L.Y., Jan Y.N.;
RA "Miranda is required for the asymmetric localization of Prospero
RT during mitosis in Drosophila.";
RL Cell 90:449-458(1997).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-CANTON-S;
RA Shen C.P., Jan L.Y., Jan Y.N.;
RA Submitted (JEB-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF045771; AAC02621.1; -.
DR FlyBase: FBgn0021776; miranda.
SQ SEQUENCE 830 AA; 93172 MW; 74F80E1A4FFA1134 CPG64,

Query Match 0.6%; Score 62; DB 5; Length 830;
Best Local Similarity 46.7%; Pred. No. 4.2e+02;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Q7 1176 TVGKPPKMKQKKSQLESVQVGGSYWQ 1205
Db 402 TEQQAVAKVQQVESDESAREKSYWR 431
|||||
|||||

RESULT 172
09LKC1 PRELIMINARY; PRT; 836 AA.
AC 09LKC1;
DT 01-OCT-2000 (TRENBLREL 15, Created)
DT 01-OCT-2000 (TRENBLREL 15, Last sequence update)

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DI 01-MAY-1997 (TrEMBLrel. 15, last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 15, last annotation update)
DE ALPHA-KETOGLOUTARATE DEHYDROGENASE.
EN SUCA.
OS Bradyrhizobium japonicum.
OC bacteria, Proteobacteria, alpha subdivision, Rhizobiales group:
OX NCBL_taxID=375;
KN [1]
RN SEQUENCE FROM N.A.
RC STRAIN USDA110;
RX MEDLINE-97136621; PubMed 8981998;
RA Green L.S., Emerich D.W.;
PI "Bradyrhizobium japonicum does not require alpha-ketoglutarate
PI dehydrogenase for growth on succinate or malate.";
KL J. Bacteriol. 179:194-201(1997).
DR EMBL: U7618; AAC44748.1;
DR InterPro: IPR001017;
DR Pfam: PF00676; EL_dehydrog; 1.
SO SEQUENCE 965 AA; 110920 MW; 5AD4E97A8EFH4280 chr64;

Query Match. 9.64; Score 62; DB 10; Length 965;
Best Local Similarity 43.48; Pred. No. 5,1e-02;
Matches 13; Conservative 6; Mismatches 11; Gaps 0;

Q7 1774 EFISPYIEGII SQVILPKITSPM SASQA 1802
DI 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DI 01-MAY-2001 (TrEMBLrel. 16, last annotation update)
DE TKR PROTEIN (TKR-III PROTEIN).
EN TER-03 G2672;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota, Metazoa, Arthropoda, Tracheata, Insecta;
OC Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha;
OX NCBL_taxID=7227;
KN [1]
RN SEQUENCE FROM N.A.
RC STRAIN BERKELEY;
RX MEDLINE-20196006; PubMed 10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gockyne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
RA Sultun G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Hlazo R.G., Champ M., Pfeiffer R.D.,
RA Wan F., Joyly R., Mayro F., Hsu C., Nelson C.W., Mayes G.L.G.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Plankoch C., Baldwin L.,
RA Ballou K.M., Basa A., Baxendale J., Kuytakaralia L., Keasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadion E., Center A., Chandra L.,
RA Cherry J.M., Cawley S., Dahke C., Daynoff L.B., Davies P.,
RA de Fabios R., Delcher A., Deng Z., Dey S.A., Jew L., Dietz S.M.,
RA Dodson K., Doup L.E., Downes K., Egan R.C., Eick J., Dunn P.,
RA Egan K.I., Evangelista C., Foray C., Forster S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garb N.S., Gelbart W.M., Glasser K.,
RA Gleider K., Gura F., Gurell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.H., Harvey D., Helman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeaw C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Korchum K.A.,
RA Kimmel B.E., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.B., Li J., Li Z., Liang Y., Liu X.,
RA Liu X., Martel B., McIntosh T.C., Melov M.P., McIntosh D.,
RA Merkulov G., Milshina N.V., McBarry C., Morris J., Moshrefi A.,

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DI 01-MAY-1997 (TrEMBLrel. 15, last annotation update)
DI 01-MAY-2000 (TrEMBLrel. 15, last annotation update)
DE ALPHA-KETOGLOUTARATE DEHYDROGENASE.
EN SUCA.
OS Bradyrhizobium japonicum.
OC bacteria, Proteobacteria, alpha subdivision, Rhizobiales group:
OX NCBL_taxID=375;
KN [1]
RN SEQUENCE FROM N.A.
RC STRAIN USDA110;
RX MEDLINE-97136621; PubMed 8981998;
RA Green L.S., Emerich D.W.;
PI "Bradyrhizobium japonicum does not require alpha-ketoglutarate
PI dehydrogenase for growth on succinate or malate.";
KL J. Bacteriol. 179:194-201(1997).
DR EMBL: U7618; AAC44748.1;
DR InterPro: IPR001017;
DR Pfam: PF00676; EL_dehydrog; 1.
SO SEQUENCE 965 AA; 110920 MW; 5AD4E97A8EFH4280 chr64;

Query Match. 9.64; Score 62; DB 10; Length 965;
Best Local Similarity 43.48; Pred. No. 5,1e-02;
Matches 13; Conservative 6; Mismatches 11; Gaps 0;

Q7 1774 EFISPYIEGII SQVILPKITSPM SASQA 1802
DI 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DI 01-MAY-2001 (TrEMBLrel. 16, last annotation update)
DE TKR PROTEIN (TKR-III PROTEIN).
EN TER-03 G2672;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota, Metazoa, Arthropoda, Tracheata, Insecta;
OC Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha;
OX NCBL_taxID=7227;
KN [1]
RN SEQUENCE FROM N.A.
RC STRAIN BERKELEY;
RX MEDLINE-20196006; PubMed 10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gockyne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
RA Sultun G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Hlazo R.G., Champ M., Pfeiffer R.D.,
RA Wan F., Joyly R., Mayro F., Hsu C., Nelson C.W., Mayes G.L.G.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Plankoch C., Baldwin L.,
RA Ballou K.M., Basa A., Baxendale J., Kuytakaralia L., Keasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadion E., Center A., Chandra L.,
RA Cherry J.M., Cawley S., Dahke C., Daynoff L.B., Davies P.,
RA de Fabios R., Delcher A., Deng Z., Dey S.A., Jew L., Dietz S.M.,
RA Dodson K., Doup L.E., Downes K., Egan R.C., Eick J., Dunn P.,
RA Egan K.I., Evangelista C., Foray C., Forster S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garb N.S., Gelbart W.M., Glasser K.,
RA Gleider K., Gura F., Gurell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.H., Harvey D., Helman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeaw C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Korchum K.A.,
RA Kimmel B.E., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.B., Li J., Li Z., Liang Y., Liu X.,
RA Liu X., Martel B., McIntosh T.C., Melov M.P., McIntosh D.,
RA Merkulov G., Milshina N.V., McBarry C., Morris J., Moshrefi A.,

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DR EMBL: Z81074; CAB03036.1;
 SSO SEQUENCE 278 AA; 36948 MW; 08E1E19E501F962E CRC64;

Query Match
 Best Local Similarity 22.4%; Pred. No. 1,560;2;
 Matches 15; Conservative 13; Mismatches 39; Indels 0; Gaps 0;

QY 256 PEEAATYMTTETSVVTEHTNTHVSLASATPTPTPTSLTEGCTSLVLDLQKQKES 315
 DB 23 EEPFIVVIVIVVERAKPTALNFVSTFWITPTATPTATPTATPTATPTATPTATPTAT 82
 QY 315 LKKEPP 322
 DB 83 VTUSVP 89

RESULT 169
 QY 456 PRELIMINARY; PRT: 296 AA.
 AC Q93456;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE F1028.7 PROTEIN.
 GN F1028.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Phabditidae;
 OC Rhabditidae; Poloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 [1]
 SEQUENCE FROM N.A.
 RA Basham V.;
 RA Submitted (SEF 1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

SEQUENCE FROM N.A.
 MEDLINE-04150738; PubMed 7905498;
 RA Wilson R., Ainsworth K., Anderson K., Baynes C., Berks M.,
 Bentley J., Burton J., Gensell M., Gopsey T., Cooper J., Coulson A.,
 Clouston M., Dear S., De Zee, Durbin K., Eaves A., Fulton D.,
 Gardner A., Green P., Hawkins T., Hillier S., Jier M., Johnston L.,
 Jones M., Kershaw P., Kingston J., Laister N., Latreille P.,
 Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Picken L., Raza A., Saunders D., Searles E.,
 Smalton N., Smith A., Southam E., Staden R., Sulston J.,
 Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 Watson M., Weinstock L., Wilkinson S., Spratt J., Wohlman P., Telford
 RT Nature 368:32-38(1993).
 RT Nature 360:216-284(1993).
 DR EMBL: Z80216; CAB02283.1;
 DR InterPro: IPR000445;
 DR SEQUENCE 295 AA; 43614 MW; APTF594221881BA CRC64;

Query Match
 Best Local Similarity 26.7%; Pred. No. 1,860;2;
 Matches 12; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1522 FVVVSTZPHLPLGLHPLFLVGVAVAGQVETFAATVST 1576
 DB 210 FFAVAVAGQVETFAATVST 210

RESULT 190
 QY 600 PRELIMINARY; PRT: 298 AA.
 AC Q96000;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE D11903B.F11COLLINEAR SYNTHETASE.
 GN D11903B.F11COLLINEAR SYNTHETASE.
 OS CAFA.

Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
 OC Zymomonas.
 NCBI_TaxID=542;
 [1]
 SEQUENCE FROM N.A.
 RA Lee J.S., Kang H.S.;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN EMBL: AF117451; AAF13753.1;
 DR InterPro: IPR002220;
 DR Pfam: PF00761; DHDFS; 1;
 DR PRINTS: PR00146; DHPICSNTHASE.
 DR SEQUENCE 299 AA; 33180 MW; 3A12C038453FE11 CRC64;

Query Match
 Best Local Similarity 28.5%; Pred. No. 1,860;2;
 Matches 16; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 657 TGVNQKMIELLADNINLQDPSMILKMWDELISVCHFFPSNLPQVTFVVIIV 712
 DB 76 TGAFTPTDILLSEQLQKSGVSALLPLVSYHALNDEVSIVETVSKHVSVIV 131

RESULT 191
 QY 619 PRELIMINARY; PRT: 322 AA.
 AC Q9VD19;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CARNITINE AMYLASE (EC 4.2.1.1) (CAPRONATE DEHYDRATASE)
 GN CG5379.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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 MEDLINE 20190036; PubMed 10731132;
 RA Adams M.D., Celinker S.E., Holt F.A., Evans C.A., Gacyne T.D.,
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 Nelson P.P., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 Palazzone M., Pittman G.S., Pan S., Pollard J., Puci V., Reese M.G.,
 Reinert S., Remington K., Saunders F.P.C., Scheeler P., Shen H.,
 Shure R.C., Sidon-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Fri Nov 9 15:42:42 2001

Best Local Similarity 30.2%, Pred. No. 2,200,02;
Matches 13; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1472 KLPEKEETIPKAVSFNFSQPFMIQVENVETHTSKQIPHEK 1514
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||| :
Db 172 KLPGGGGQSPGQIVSAPEKPKPEPPQIKQGLKPMQKQIPQLQ 214

Search Completed: December 6, 2001, 12:24:51
Job time: 278 sec

R:Geisler, N.; Weber, K.
EMBO J. 7, 15-20, 1988
A:Title: Phosphorylation of desmin in vitro inhibits formation of intermediate filament
A:Reference number: S02448; M01D:88196075
A:Accession: S02448
A:Molecule type: protein
A:Residues: 1-69 <OE2>
R:Kitamura, S.; Ando, S.; Shibata, M.; Tanabe, K.; Sato, C.; Inagaki, M.
J. Biol. Chem. 264, 5674-5678, 1989
A:Title: Protein kinase C phosphorylation of desmin at four serine residues within the
A:Reference number: A42858; M01D:89174618
A:Accession: A42858
A:Molecule type: protein
A:Residues: 1-10 14,28 42,59 59 <KIT>
R:Geisler, N.; Schuenemann, J.; Weber, K.
Eur. J. Biochem. 206, 841-852, 1992
A:Title: Chemical cross-linking indicates a staggered and antiparallel protofilament
A:Reference number: S23189; M01D:92299013
A:Accession: S23189
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 14,25 256,274 282,293-301 <EP>
C:Comment: This protein was isolated from chicken gizzard.
C:Comment: There appears to be a single desmin gene in the haploid chicken genome. The
predominantly in skeletal, cardiac, and most types of smooth muscle cells during myoblast
C:Comment: Desmin intermediate filaments are found in the cytoplasm of cultured myoblasts
C:Comment: The molecule contains three structurally distinct domains. The surface-exposed
The tailpiece comprises the carboxyl terminal residues.
C:Suprafamily: cytoskeletal keratin
C:Keywords: blocked amino end; coiled coil; intermediate filament; muscle; phosphoprotein
F:1-99/Domain: head <HED>
F:100-467/Domain: rod <ROD>
F:100-132/Region: coil 1A
F:133-142/Region: linker 1
F:143-243/Region: coil 1B
F:244-259/Region: linker 12
F:260-278/Region: coil 2A
F:279-286/Region: linker 2
F:287-407/Region: coil 2B
F:345/Region: stutter
F:408-463/Domain: tail <ETD>
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F:6-22/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status experimental
F:12,29,38,59/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental
F:29,35,59/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experimental
F:64/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status experimental

Query Match 0.7%; Score 74; DB 1; Length 463;
Best local similarity 30.4%; Pred. No. 2.6;
Matches 24; Conservative
QY 2961 LWRPLNVTTLTKTFSSKVFQAAALFWALAKLEKENVIVLLESIFELALHMEYCEP 2120
DB 181 LKQKIGLEIGLKQEAERHAAFNADVDAATLAKILLESIESLFFIAFKVIREELINE 240

QY 2121 VEHQCKRTIOOLETVIRP 2139
DB 241 IQAALQEQHILQVEMDISAP 259

RESULT 8
DMHU
desmin - human
N:Alternate names: type III intermediate filament
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 10-Dec-1999
C:Accession: J00063
R:Li, Z.; Lieberbaum, A.; Butler-Browne, G.; Paulin, D.
Gene 78, 243-254, 1989
A:Title: Human desmin-coding gene, complete nucleotide sequence, characterization and
A:Reference number: J00063; M01D:89378751

Query Match 0.7%; Score 76; DB 2; Length 3144;
Best local similarity 36.7%; Pred. No. 14;
Matches 18; Conservative
QY 1462 SLMMNLYLLELEPEKEETTPAVSNKSPKPMQVNVFTHSKOL 1510
DB 2227 SLNNAQSELTINPKPTTPSESEKREKSNPAPTPKTFWSSRL 2275

RESULT 6
T07648
hypothetical protein TIP17.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 22-Oct-1999
C:Accession: T07648
R:Kobayashi, M.; Peters, S.A.; van Slamat, M.; Sirkko, W.; Stokkoma, W.; Bancroft, I.; New
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15790
A:Accession: T07648
A:Molecule type: DNA
A:Residues: 1-138 <DPY>
A:Cross-references: EMBL:AL049730; GSPDB:G000662; ATSP:TIP17.150
A:Experimental source: cultivar Columbia; BAC clone TIP17
C:Genetics:
A:Gene: ATSP-TIP17 150
A:Map position: 4

Query Match 0.7%; Score 74; DB 2; Length 408;
Best local similarity 32.6%; Pred. No. 2.2;
Matches 14; Conservative
QY 723 FPAIRVFSLLQKKIKLESVITAVEIPSEWHITMLDRCTP 765
DB 171 FPEVKEVSEFPFNSWPTESVA-SFQITFEYVHIFRGGCV 213

RESULT 7
DMCH
desmin - chicken
N:Alternate names: type III intermediate filament
C:Species: Gallus gallus (chicken)
C:Date: 18-Dec-1981 #sequence_revision 12-Apr-1996 #text_change 10-Dec-1999
C:Accession: A90469; A94014; J01459; S02448; A42858; S23189; A02957
R:Geisler, N.; Weber, K.
EMBO J. 1, 1649-1656, 1982
A:Title: The amino acid sequence of chicken muscle desmin provides a common structural
A:Reference number: A90469; M01D:84297925
A:Accession: A90469
A:Molecule type: protein
A:Residues: 1-463 <GET>
R:Capitani, Y.G.; Ngai, T.; Lazarides, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 6909-6913, 1984
A:Title: Characterization and regulation in the expression of a gene coding for the inter-
A:Reference number: A94014; M01D:85063701
A:Accession: A94014
A:Molecule type: mRNA
A:Residues: 366-463 <CAP>
R:Gusella, J.F.; Matsuyama, Y.; Tsubimura, K.; Ito, H.; Ando, S.; Kamijo, M.; Yasuda, H.;
Biochem. Biophys. Res. Commun. 190, 927-934, 1993
A:Title: cdc2 kinase phosphorylation of desmin at three serine/threonine residues in the
A:Reference number: J01459; M01D:93176201
A:Accession: J01459
A:Molecule type: protein
A:Residues: 5,9,16-27,63 67 <KES>

111

A:Accession: A24783
 A:Molecule type: DNA
 A:Residues: 1-469 <DNA>
 A:Cross-references: GDB:M12104; NID:3191360; PIDN:AAA37072.1; PID:9387071
 C:Genetics:
 A:Title: The 3' region of the 26S subunit of the 65 kDa subunit of protein phosphatase 2A have a signal peptide
 C:Keywords: cytoskeletal keratin

Query Match 0.6% Score 70; DB 2; Length 469;
 Best Local Similarity 29.3%; Pred. No. 8.8;
 Matches 22; Conservative 13; Mismatches 40; Indels 0; Gaps 0;
 QY 2065 LNYGTHLFFHSSKFFVPAALITVLAIAAEKIKRYIVLIESITFLAEAMQDCEFEVHQ 2124
 DB 193 LQEFQIGRFAENLAAPRAVDAAATLADIDLEKRIEENLILAKKVIHREIPFLQAG 252
 QY 2125 GQRTTQQLFTVLGEP 2149
 DB 253 LQEGQGVQVEMMSKP 267

RESULT 21
 A54104
 desmin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Apr-1994 #sequence_revision 92 A:q-1994 #text_change 19-Apr-1996
 A:Accession: A54104; S1404
 R:Title: H.; Choudhury, S.K.; Milner, D.J.; Munir, M.I.; Kuisk, I.R.; Capetanaki, Y.
 J. Cell Biol. 124: 927-941, 1994
 A:Title: Inhibition of desmin expression blocks myoblast fusion and interferences with the
 A:Reference number: A54104; MUID:94165148
 A:Accession: A54104
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-469 <DNA>
 A:Cross-references: GB:I22550
 R:Title: H.; Capetanaki, Y.
 submitted to the EMU data library, December 1992
 A:Description: Regulation of the Mouse Desmin Gene: Transactivation by MyoD, Myogenin,
 A:Reference number: S31404
 A:Accession: S31404
 A:Molecule type: DNA
 A:Residues: 1-40 <DNA>
 A:Cross-references: DMB:216992
 C:Superfamily: cytoskeletal keratin
 C:Keywords: muscle

Query Match 0.6% Score 70; DB 2; Length 469;
 Best Local Similarity 29.3%; Pred. No. 8.8;
 Matches 22; Conservative 13; Mismatches 40; Indels 0; Gaps 0;
 QY 2065 LNYGTHLFFHSSKFFVPAALITVLAIAAEKIKRYIVLIESITFLAEAMQDCEFEVHQ 2124
 DB 193 LQEFQIGRFAENLAAPRAVDAAATLADIDLEKRIEENLILAKKVIHREIPFLQAG 252
 QY 2125 GQRTTQQLFTVLGEP 2149
 DB 253 LQEGQGVQVEMMSKP 267

RESULT 22
 B34541
 phosphoprotein phosphatase 2-beta regulatory chain - human
 R:Alternate names: phosphoprotein phosphatase 2A-beta 65K regulatory chain
 C:Species: Homo sapiens (man)
 C:Date: 29-Jun-1990 #sequence_revision 29-Jun-1990 #text_change 13-Sep-1998
 A:Accession: B34541
 R:Description: B.A. Adams-Pearson, C. Maurer, F. Mueller, P. Coris, J. Merlevede, W.
 Biochemistry 29: 4166-4173, 1990
 A:Title: Alpha- and beta-forms of the 65-kDa subunit of protein phosphatase 2A have a signal

A:Reference number: A34541; MUID:90241887
 A:Accession: B34541
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-571 <HPM>
 A:Cross-references: GR M65254; NID:9189429
 C:Genetics:
 A:Gene: GDB:PTP2R1B
 A:Cross-references: GDB:136799
 C:Superfamily: phosphoprotein phosphatase 65K regulatory chain

Query Match 0.6% Score 69; DB 2; Length 571;
 Best Local Similarity 22.2%; Pred. No. 15;
 Matches 16; Conservative 20; Mismatches 36; Indels 0; Gaps 0;
 QY 2067 YQILKTRISSPRVFAALITVLAIAAEKIKRYIVLIESITFLAEAMQDCEFEVHQ 2126
 DB 269 IQNLEDCAEVFAAAAAHKKVFIENIPEDREPTIMNOILPVILKELVSDTNGVRSALA 328
 QY 2127 KTQQLFTVLGE 2138
 DB 329 SVIMGLSTIIIGK 340

RESULT 23
 A96732
 unknown protein F5A18.7 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 A:Accession: A96732
 R:Description: A. Escher, J.K.; Fajal, G.; Fiederspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.P.; Conway, P.H.; Dwyer
 Ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 409: 876-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Liu, J.H.; Liu, Y.; Liu, S.X.; Liu, Z.A.; Loh, S.; Maiti, P.; Marti
 Rizzo, M.; Rooney, T.; Rowley, P.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, B.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: A96732
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-749 <STG>
 A:Cross-references: GB:AF005173; NID:96453826; FLN:AAF05669.1; GSP:BB-GN00141
 C:Genetics:
 A:Gene: F5A18.7
 A:Map position: 1

Query Match 0.6% Score 69; DB 2; Length 749;
 Best Local Similarity 23.9%; Pred. No. 21;
 Matches 17; Conservative 21; Mismatches 33; Indels 0; Gaps 0;
 QY 1247 KKKLPELQGVVFLNLTSPITFLAEAMQDCEFEVHQ 1276
 DB 350 ETEFFKIVITETKMPVLTINLEKRIEENLILAKKVIHREIPFLQAG 409
 QY 1277 ILDEKFNVEL 1287
 DB 410 VLTVDKKEEL 420

RESULT 24
 D71372
 conserved hypothetical protein TP0050 - Syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 06-Nov-1999
 A:Accession: D71372
 R:Fraser, C.M.; Norris, S.J.; Winslock, G.M.; White, O.; Sutton, G.; Jackson, R.; G
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M

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DOI: 10.1177/1056492613505111
<http://jmi.sagepub.com>

A:Title: Nucleotide sequence of a Bacillus megaterium gene homologous to the dnaK gene
A:Reference number: 139837; MUID:87231083
A:Accession: 139837
A>Status: preliminary; translated from GR/IMMUNOLOGY
A:Molecule type: DNA
A:Residues: 1-605 <RES>
A:Cross-references: GB:M31338; NID:q39628; PID:q39629
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 0.6%; Score 64; DB 2; Length 605;
Best Local Similarity 32.7%; Pred. No. 74; Indels 0; Gaps 0;
Matches 17; Conservative 12; Mismatches 23
QY 54R FSSEVTISRLNIFQAPISYNFWYFVIFIAAPTEIKETISENDSNOV 599
DB 514 FTTEKTLKDLGKVEAEVYANFADAKAATFKNMFFKAKKDTQIV 565
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 0.6%; Score 64; DB 2; Length 771;
Best Local Similarity 36.1%; Pred. No. 97; Indels 0; Gaps 0;
Matches 13; Conservative 10; Mismatches 13
QY 639 GWEPATFNVITKTRPKITGVANOKMIFETLAPNTNL 674
DB 487 GWKALGSLNEPFAEGRKIGRENERPCILLDELDV 522
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 0.6%; Score 64; DB 2; Length 771;
Best Local Similarity 36.1%; Pred. No. 97; Indels 0; Gaps 0;
Matches 13; Conservative 10; Mismatches 13
QY 639 GWEPATFNVITKTRPKITGVANOKMIFETLAPNTNL 674
DB 487 GWKALGSLNEPFAEGRKIGRENERPCILLDELDV 522
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 0.6%; Score 64; DB 2; Length 771;
Best Local Similarity 36.1%; Pred. No. 97; Indels 0; Gaps 0;
Matches 13; Conservative 10; Mismatches 13
QY 639 GWEPATFNVITKTRPKITGVANOKMIFETLAPNTNL 674
DB 487 GWKALGSLNEPFAEGRKIGRENERPCILLDELDV 522
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 0.6%; Score 64; DB 2; Length 771;
Best Local Similarity 36.1%; Pred. No. 97; Indels 0; Gaps 0;
Matches 13; Conservative 10; Mismatches 13
QY 639 GWEPATFNVITKTRPKITGVANOKMIFETLAPNTNL 674
DB 487 GWKALGSLNEPFAEGRKIGRENERPCILLDELDV 522
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 0.6%; Score 64; DB 2; Length 771;
Best Local Similarity 36.1%; Pred. No. 97; Indels 0; Gaps 0;
Matches 13; Conservative 10; Mismatches 13
QY 639 GWEPATFNVITKTRPKITGVANOKMIFETLAPNTNL 674
DB 487 GWKALGSLNEPFAEGRKIGRENERPCILLDELDV 522
A:Accession: G71409
A:Reference number: A71400; MUID:98121113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <REV>
A:Cross-references: GB:297336; NID:q224788; PID:q224826
C:Genetics:
A:Map position: 4COP9-4G3845

A:Gene: spoIIIE

Query Match 0.6%; Score 64; DB 2; Length 789;
Best Local Similarity 33.3%; Pred. No. 99; Indels 0; Gaps 0;
Matches 13; Conservative 8; Mismatches 18
QY 1470 LKLPKPEETIPKAVSPNKSEQEMLOVFNVEHHSK 1508
DB 323 LKLPNNPNOSMEKRLILKNAKRLKLTLESFGVKAHVK 361
A:Accession: F75372
A:Reference number: A75250; MUID:20036896
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-799 <WHI>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain R1
C:Genetics:
A:Gene: Dri629
A:Map position: 1

Query Match 0.6%; Score 64; DB 2; Length 790;
Best Local Similarity 34.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 17; Conservative 9; Mismatches 24
QY 1190 SQPLESVQGVGGSYQWQVILLILALQHKKLLKSPQILVPTLILNLSRCLE 1239
DB 207 SLNACVQGLSGGTSAAATITTFPALPHAKTVASPRYKSVLPHFSQLILD 256
A:Accession: D70128
A:Reference number: A70100; MUID:98065943
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-971 <P>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain B31

Query Match 0.6%; Score 64; DB 2; Length 790;
Best Local Similarity 34.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 17; Conservative 9; Mismatches 24
QY 1190 SQPLESVQGVGGSYQWQVILLILALQHKKLLKSPQILVPTLILNLSRCLE 1239
DB 207 SLNACVQGLSGGTSAAATITTFPALPHAKTVASPRYKSVLPHFSQLILD 256
A:Accession: D70128
A:Reference number: A70100; MUID:98065943
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-971 <P>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain B31

Query Match 0.6%; Score 64; DB 2; Length 971;
Best Local Similarity 34.1%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 9; Mismatches 18
QY 61 SFEQPEAPLFSQAKTLERSVQTKAVNKOLDENISLFIHL 101
DB 839 SFASYRDPNFTTYQAFKSELELANNNKMTDDEIYTLIGL 879
A:Accession: D70128
A:Reference number: A70100; MUID:98065943
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-971 <P>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain B31

Query Match 0.6%; Score 64; DB 2; Length 971;
Best Local Similarity 34.1%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 9; Mismatches 18
QY 61 SFEQPEAPLFSQAKTLERSVQTKAVNKOLDENISLFIHL 101
DB 839 SFASYRDPNFTTYQAFKSELELANNNKMTDDEIYTLIGL 879
A:Accession: D70128
A:Reference number: A70100; MUID:98065943
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-971 <P>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain B31

Query Match 0.6%; Score 64; DB 2; Length 971;
Best Local Similarity 34.1%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 9; Mismatches 18
QY 61 SFEQPEAPLFSQAKTLERSVQTKAVNKOLDENISLFIHL 101
DB 839 SFASYRDPNFTTYQAFKSELELANNNKMTDDEIYTLIGL 879
A:Accession: D70128
A:Reference number: A70100; MUID:98065943
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-971 <P>
A:Cross-references: GB:A830207; NID:q456403; PID:A830207
A:Experimental source: strain B31

[illegible]

Query Match 0.6%; Score 61; DB 1; Length 270;

Gaps: 0;

0002-11

100

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29
30
31

6661-1.

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A:Map position: 2
 C:Superfamily: protein kinase family, SAM homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:1-66/Domain: SAM homology <SAM>
 F:392-658/Domain: protein kinase homology <KIN>
 F:400-408/Region: protein kinase ATP-binding motif

Query Match 0.6%; Score 61; DB 1; Length 659;
 Best Local Similarity 30.6%; Pred. No. 2; 02;
 Matches 15; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

QY 1579 AILSKAVLLAVKALITETITLVKGVCHPLQVVERKALDLELNLK 1627
 DB 170 AALSSQSSISPLSSVLTSTKFSVFSNANSTFTSTQAPFGHHSK 218

RESULT 134
 S66699
 hypothetical protein Y01017w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein Q2321
 C:Species: Saccharomyces cerevisiae
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
 C:Accession: S66699
 R: Hughes, B.; Pohl, T.M.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66685
 A:Accession: S66699
 A:Molecule type: DNA
 A:Residues: 1-714 <100>
 A:Cross-references: EMBL:274757; NID:3119793; PID:3119793; 35496-390601
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: MIPS:Y01017w
 A:Map position: 151

Query Match 0.6%; Score 61; DB 2; Length 714;
 Best Local Similarity 17.4%; Pred. No. 2; 02;
 Matches 15; Conservative 18; Mismatches 53; Indels 0; Gaps 0;

QY 1451 CCFPSVQHQVQSMLNHIYLLKPEEKEETIPKAVSNKSEQEMIQVNVHTSKOL 1510
 DB 469 CCAVGTGAGFESYSGYVKEEELTEILAKTAKEHQLKILYFETPACTFELQV 759

QY 1511 RHKKFISVSPMSLSNNHLEKAVE 1536
 DB 529 NMVIFAEVPIHFVAGDSLSNPIE 554

RESULT 134
 JE0269
 Proxi protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0269
 R:Tomarev, S.I.; Zisovitcha, E.D.; Chang, R.; Hines, R.I.
 Biochem. Biophys. Res. Commun. 249: 884-889, 1998
 A:Title: Characterization of the mouse Proxi gene.
 A:Reference number: JE0269; MUID:98369610
 A:Accession: JE0269
 A:Molecule type: mRNA
 A:Residues: 1-737 <100>
 A:Cross-references: GB:AF066576; NID:33452316; UDR:AAC326-4...; EID:33452317
 C:Genetics:
 A:Gene: Proxi
 A:Map position: 1
 A:Introns: 5753; 61173; 67673

Query Match 0.6%; Score 61; DB 2; Length 737;
 Best Local Similarity 40.2%; Pred. No. 2; 30-02;
 Matches 13; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1472 KIPFPERPTPKAVSNKSEQEMIQVNVHTSKOLRHEK 1514
 DB 212 KIPFPERPTPKAVSNKSEQEMIQVNVHTSKOLRHEK 254

RESULT 135
 T48463
 hypothetical protein TIE3.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-2000 #sequence_revision 23-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48463
 R:Kavan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Passoville, R.; De Clerck, E.;
 Eves, H.W.; Rudd, S.; Lemcke, K.; Mayer, Z.P.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224491
 A:Accession: T48463
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-766 <100>
 A:Cross-references: EMBL:AL162972
 A:Experimental source: cultivar Columbia; HAC clone TIE3
 C:Genetics:
 A:Map position: 5
 A:Introns: 2177; 4527; 49271
 A:Note: TIE3.30

Query Match 0.6%; Score 61; DB 2; Length 766;
 Best Local Similarity 37.5%; Pred. No. 2; 40-02;
 Matches 13; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 814 NPQLKEDSDYLLHLIGLFEMMINGSADAVHF 845
 DB 571 NQKMLEDDQYLQLOKRAPELMIDGPEKYHF 602

RESULT 136
 VPXW5
 outer layer protein VP3 - human rotavirus A (serotype 3 strain P)
 N:Alternate names: hemagglutinin
 C:Species: human rotavirus A
 C:Date: 30-Nov-1999 #sequence_revision 30-Nov-1999 #text_change 01-Mar-1996
 C:Accession: C28839
 R:Corbitt, M.; Green, K.; Nishikawa, K.; Taniguchi, K.; Jones, P.; Kapikian, A.Z.;
 J. Virol. 62: 2978-2984, 1988
 A:Title: Sequence of the fourth gene of human rotaviruses recovered from asymptomatic
 A:Reference number: A28839; MUID:88275070
 A:Accession: C28839
 A:Molecule type: genomic RNA
 A:Residues: 1-775 <100>
 C:Genetics:
 A:Map position: segment 4
 C:Superfamily: rotavirus outer layer protein VP3
 C:Keywords: capsid protein; coat protein; glycoprotein; hemagglutinin
 F:1-241/Region: outer capsid protein VP8 #status predicted <VP8>
 F:241-246/Region: cleavage processing #status predicted
 F:247-775/Region: outer capsid protein VP5 #status predicted <VP5>
 F:327-557/Region: outer capsid protein VP6 #status predicted <VP6>
 F:557-775/Region: outer capsid protein VP7 #status predicted <VP7>

Query Match 0.6%; Score 61; DB 1; Length 775;
 Best Local Similarity 30.2%; Pred. No. 2; 40-02;
 Matches 16; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

QY 1045 IQRETTAVLKDEAMVLLTICKYNEFSVLLNEDPKSLDIPKAVHTTKELXA 1097
 DB 667 LPKASYKALKDDEWMEINIEGFFAYKIDITLNEVFEDVKNKTEIVTNIPVISA 719

RESULT 137
 T38016

C:Superfamily: unassigned ATP-binding cassette proteins: ATP-binding cassette homolog

Query Match 0.6%; Score 60; DB 2; Length 544;
 Best Local Similarity 27.9%; Pred. No. 2.2e+02;
 Matches 17; Conservative 10; Mismatches 34; Indels 0; Gaps 0;

QY 1040 QLEKIQEPTAVLKDEAVMLHLTLGKYNEFSVSLNEPKSLDIFIKAVHHTKELYACM 1099
 DB 272 QRMVETKPEPRVAVKLEPAVTAQASACKYPIIMHFFKLAGAKERLDDAVEAVRDETRVDL 331
 QY 1100 P 1100
 DB 332 P 332

RESULT 170
 A45624
 trophozoite cysteine proteinase - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000
 C:Accession: A45624
 P:Bossenbal, P.J.; Nelson, R.G.
 Mol. Biochem. Parasitol. 51, 143-152, 1992
 A:Title: Isolation and characterization of a cysteine proteinase gene of Plasmodium f
 A:Reference number: A45624; X010:92228005
 A:Accession: A45624
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 559; P03
 A:Cross-references: GB:M81341; GB:M85550; NID:J169247; PIDN:AAA9578.1; PID:q160248
 A:Note: sequence extracted from RCH1 backbone (NCBIN:98870, NCBI:P:98874)
 C:Superfamily: trophozoite cysteine proteinase

Query Match 0.6%; Score 60; DB 2; Length 544;
 Best Local Similarity 23.1%; Pred. No. 2.3e+02;
 Matches 15; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

QY 390 NNLHLLASLLFEYISYSSOEEMDSKVSLLNQPLRLLESKYPRTLDDVLEPHLK 449
 DB 162 MPTFEKYTLINSETYNNKHWVSNIKNSFKSTKSPFEYINLFFILPKYKFFTFNNNEPFRK 161
 QY 450 ELADL 454
 DB 162 ELSNI 166

RESULT 171
 D34541
 phosphotriester phosphatase (E.C.3.1.3.16) 2A-beta 65K regulatory chain - P19 (fragment
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 29-Jun-1990 #sequence_revision 23-Jun-1990 #text_change 24-Sep-1999
 C:Accession: D34541
 P:Hemmings, R.A.; Adams-Pearson, C.; Maurer, F.; Mueller, F.; Goris, J.; Morley, W
 Biochemistry 29, 3165-3173, 1990
 A:Title: Alpha- and beta-forms of the 65-kDa subunit of protein phosphatase 2A have a
 A:Reference number: A34541; M010:90241887
 A:Accession: D34541
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-602; JHEM
 A:Cross-references: GB:734931; NID:q510346; PIDN:CAA84403.1; PID:q510347
 C:Superfamily: phosphotriester phosphatase 65K regulatory chain
 C:Keywords: phosphoric monoester hydrolase

Query Match 0.6%; Score 60; DB 2; Length 602;
 Best Local Similarity 22.2%; Pred. No. 2.4e+02;
 Matches 16; Conservative 18; Mismatches 36; Indels 0; Gaps 0;

QY 2067 YOLLKTPHSSPKVFAALLIVLALAEKLENTIVLLPESIFPLAEELMEDICEEVHQCC 2126
 DB 1111

A:Residues: 1-541 <ARN>
 A:Cross-references: GB:AE061648; GB:AE061663; NID:q4376946; PIDN:AA018792.1; PID:q437695
 A:Experimental source: strain CWI029
 P:Reed, T.D.; Brunkham, R.C.; Shen, C.; Gill, S.R.; Heideberger, J.F.; White, G.; Hickey,
 C.; Jackson, R.; Gwin, M.; Nelson, M.; DeBorja, K.; Kelland, J.; McClarty, G.; Saito, T.;
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; M010:20150255
 A:Accession: B81500
 A:Molecule type: DNA
 A:Residues: 1-541 <REA>
 A:Cross-references: GB:AE061672; GB:AE061671; NID:J1899318; PIDN:AA037978.1; PID:q718902
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: cutE; CP00094
 C:Superfamily: apolipoprotein N-acyltransferase

Query Match 0.6%; Score 60; DB 2; Length 541;
 Best Local Similarity 33.3%; Pred. No. 2.2e+02;
 Matches 13; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 271 MRHFPVNSLASQITETITETISLKEGCSLIVLTPQK 312
 DB 74 LSDQYICKLIVLVMLILITISLVLSGSGSILVAIVQK 112

RESULT 168
 B86572
 apolipoprotein N-acyltransferase [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: B86572
 P:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
 Nucleic Acids Res. 29, 2211-2214, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; M010:20340349
 A:Accession: B86572
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-541 <STO>
 A:Cross-references: GB:BA000008; NID:4897925; PIDN:BA09889.1; GSDB:GB060142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: cutE

Query Match 0.6%; Score 60; DB 2; Length 541;
 Best Local Similarity 33.3%; Pred. No. 2.2e+02;
 Matches 13; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 271 MRHFPVNSLASQITETITETISLKEGCSLIVLTPQK 312
 DB 74 LSDQYICKLIVLVMLILITISLVLSGSGSILVAIVQK 112

RESULT 169
 T35245
 Probable ABC Transporter - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
 C:Accession: T35245
 P:Roller, K.; Harris, E.; Bantley, S.E.; Parkhill, J.; Barrall, R.G.; Pajandrom, M.A
 submitted to the EMBL Data Library, April 1999
 A:Reference number: T21573
 A:Accession: T35245
 A:Status: preliminary; translated from GR/EMBL/DBP1
 A:Molecule type: DNA
 A:Residues: 1-544 <OLI>
 A:Cross-references: EMBL:AL049597; PIDN:CA040570.1; GSDB:GN00070; SC052A.03c
 A:Experimental source: strain A1(2)
 C:Genetics:
 A:Gene: SC052A.03c

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: B75055
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-643 <RAW>
A:Cross-references: GB:AF248287; GB:AF56836; NID:q3458657; FID:CAF50335.1; FID:CL51923
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1429

Query Match 0.6%; Score 60; DB 2; Length 643;
Best Local Similarity 47.6%; Pred. No. 2.7e+02;
Matches 11; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 729 PVPSILQKFKFKLESVITAVEIPSEWHIE 756
DB 136 RVMSLQAKVQRIEALKRADIPFDLEIE 164

RESULT 177
G69177
Methionine--tRNA ligase (EC 6.1.1.10) - Methanobacterium thermoautotrophicum (strain Delta H)
N:Alternate names: methionyl-tRNA synthetase
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
C:Accession: G69177
R:Smith, D.R.; Doucette Stamm, L.A.; Delouche, C.; Lee, H.; Dubois, J.; Aldredge, T.; Liu, D.; Spadafora, R.; Vicare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; K.; S.; Borge, C.M.; Borge, C.M.; Ma, T.; Piro, P.; Neill, J. N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H, found
A:Reference number: Abscon: M010:98637514
A:Accession: G69177
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-651 <MTB>
A:Cross-references: GB:AF060641; GB:AF060666; NID:q2521652; FID:AAE85093.1; FID:gnp2164
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH587

Query Match 0.6%; Score 60; DB 2; Length 651;
Best Local Similarity 35.5%; Pred. No. 2.7e+02;
Matches 11; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 647 VIKSKIKKLEGVANERKIPVLAHRIIDDP 677
DB 611 VLVLKPKAKLEPVKSPKAVIATPSENIIDDP 641

RESULT 178
S63253
Probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0505
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 20-Jun-2000
K:Messemmy, F.; Dubois, E.; Vierendeels, F.; Scherens, H.; Pierard, A.; Glandsdorff, N.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63253
A:Accession: S63253
A:Molecule type: DNA
A:Residues: 1-661 <MES>
A:Cross-references: EMBL:Z71555; FID:q1303348; FID:q1303349; GSPDB:GN06014; MIPS:YNL279w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YNL279w

A:Map position: 14L
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YNL279w
C:Keywords: Transmembrane protein
F:24-46/Domain: Transmembrane #status predicted <TM>
F:110-126/Domain: Transmembrane #status predicted <TM>
F:297-313/Domain: Transmembrane #status predicted <TM>
F:422-448/Domain: Transmembrane #status predicted <TM>
F:534-550/Domain: Transmembrane #status predicted <TM>

Query Match 0.6%; Score 60; DB 2; Length 661;
Best Local Similarity 32.2%; Pred. No. 2.7e+02;
Matches 19; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

QY 194 SLVTKSVKVPFAEYDGSASLKVLAFAIASIVSAVAALVSHIARLRIYVKGSLKES 252
DB 92 TLETLISLVIVASEGLVNFADLDLYGTYACLTIVSAVDGIVDAINTEKILISLVNDIVSS 150

RESULT 179
C71106
Hypothetical protein PH0620 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: C71106
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Se-
M.; Ohnaka, Y.; Fumihashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kusuda, R.; Omi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: C71106
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-664 <RAW>
A:Cross-references: GB:AP060603; NID:q3236130; FID:BA23709.1; FID:dic0052; FID:p32
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenB
C:Genetics:
A:Gene: PH0620

Query Match 0.6%; Score 60; DB 2; Length 664;
Best Local Similarity 37.9%; Pred. No. 2.7e+02;
Matches 11; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 728 PVPSILQKFKFKLESVITAVEIPSEWHIE 756
DB 156 PVHSLQAKVPEIFEATPRADIPFDLEIE 184

RESULT 180
T36877
Probable regulatory protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36877
R:Murphy, L.; Bartis, F.; James, K.D.; Parkhill, J.; Farrell, R.G.; Palandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21617
A:Accession: T36877
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-682 <MBP>
A:Cross-references: EMBL:AL109448; FID:q14652836.1; GSPDB:GN00070; SCOPDB:SC151.14C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SC151.14C

Query Match 0.6%; Score 60; DB 2; Length 682;
Best Local Similarity 32.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

27 456 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512
106 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512
RESULT 181
S2696
myosin heavy chain rainbow trout (trout)
C:Species: rainbow trout (trout)
C:Date: 10-Mar-1996 #sequence_revision 10-03-1996
C:Accession: S2696
Submitted to the EMBL database, March 1996
A:Description: Cloned cDNA of a fast skeletal myosin heavy chain expressed both in embryo and adult rainbow trout.
A:Reference number: S2696
A:Accession: S2696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-696
A:Accession: S2696
A:Reference number: S2696
C:Supplementary: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 0.68 Score 600 DB 2 Length 696
Best local similarity 41.04 Pred. No. 2100002
Matches 14 Conservative 0 Mismatches 14 Indels 0 Gaps 0

27 456 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512
106 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512

RESULT 182
S2696
myosin heavy chain rainbow trout (trout)
C:Species: rainbow trout (trout)
C:Date: 10-Mar-1996 #sequence_revision 10-03-1996
C:Accession: S2696
Submitted to the EMBL database, March 1996
A:Description: Cloned cDNA of a fast skeletal myosin heavy chain expressed both in embryo and adult rainbow trout.
A:Reference number: S2696
A:Accession: S2696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-696
A:Accession: S2696
A:Reference number: S2696
C:Supplementary: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 0.68 Score 600 DB 2 Length 696
Best local similarity 41.04 Pred. No. 2100002
Matches 14 Conservative 0 Mismatches 14 Indels 0 Gaps 0

27 456 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512
106 EVFTHAMHAKKEEMKESKELWKEIYKAVYASDINLQAVVIGALDAVE 512

Accession: S2696; ABB: S2696
A:Cross-references: SGD:S0000680; MIPS:YCK084c
A:Map position: 38
C:Supplementary: unassigned WD repeat proteins: WD repeat homology
C:Keywords: transcription regulation
E:97-118/Region: glutamine-rich
E:181-198/Region: glutamine-rich
E:409-422/Region: threonine-rich
E:449-452/Region: WD repeat homology WD1
E:522-556/Region: WD repeat homology WD3
E:572-605/Region: WD repeat homology WD4

Query Match 0.68 Score 600 DB 2 Length 714
Best local similarity 35.08 Pred. No. 40002
Matches 14 Conservative 10 Mismatches 16 Indels 0 Gaps 0

27 1159 GAVRLEIIEFVAVIIVVAFPPVWVFFSDFSVK 1198
DB 78 FHHVICHVPPVQIASITVQVQVQVQVQVQVQVQV 117

RESULT 183
R82944
ribosome/halactose ABC transporter (N-term domain) U0014 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #accession 20-Aug-2000
C:Accession: R82944
Submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum. Alternate views of a
A:Reference number: R82870
A:Accession: R82944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-716
A:Accession: R82944
A:Reference number: R82870
C:Experimental source: serovar 4; biovar 1
C:Genetics:
A:Gene: rbsC-1; U0014
A:Genetic code: SGD

Query Match 0.68 Score 600 DB 2 Length 746
Best local similarity 22.69 Pred. No. 410002
Matches 14 Conservative 19 Mismatches 29 Indels 0 Gaps 0

27 360 NMTHPIASTIEFFVSYSC2EMISNVSLLNEAFPLPIPIESFYPTTHAVVIEHIF 449
DB 516 HNEDELIPLVAFVPSFYASPSFYNYPIFYIYQYFNNSVILTELVRPLSIWVDEQA 575

27 450 EL 451
DB 576 QL 577

RESULT 184
V0XRM4
outer layer protein VP4 - human rotavirus A (serotype 2 strain DS1)
N:Alternate names: hemagglutinin
N:Contents: outer capsid protein VP5; outer capsid protein VP8
C:Species: human rotavirus A
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #accession 01-Mar-1996
R:Corzallia, M.; Green, K.; Nishikawa, K.; Taniguchi, K.; Jones, R.; Kapikian, A.Z.;
J. Virol. 62, 2978-2984, 1988
A:Title: Sequence of the fourth gene of human rotaviruses recovered from asymptomatic
A:Reference number: A28849; M0118625070
A:Accession: B28849
A:Molecule type: genomic RNA
A:Residues: 1-775
C:Genetics:
A:Map position: segment 4


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EMBL: Z19592; NCBI:ANN H4ED.75.
EMBL: Z19592; CAA79430.1
PIR: S4134; S4134.
SWISS-PROT: P40911; MUSE.
MOL: M01486; M01486.1.
InterPro: IPR001664;
Pfam: PF00038; Filament; 1.
PROSITE: PS00226; IF; 1.
Intermediate filament; Muscle protein.
INIT_MET 0
DOMAIN 1 107
DOMAIN 108 410
DOMAIN 411 468
DOMAIN 108 189
DOMAIN 146 149
DOMAIN 150 250
DOMAIN 251 266
DOMAIN 267 285
DOMAIN 286 293
DOMAIN 294 410
SEQUENCE 468 AA; 5366 MW; ED276; 597E4BFB CR64;

Query Match: 0.68; Score 70; DB 1; Length 468;
Best local similarity 29.38; Pred. No. 3.6;
Matches 22; Conservative 13; Mismatches 40; Gaps 0;

205 LNYQILKLEKESKPVFAALIVLALAKELFNYVLLFESTFELMELREVERHQ 214
192 LQREQLPEFAENNAAPFAVIAVLAIPPEPTESINETAFKVFHETRELOAQ 251
2125 QKTIQQLFIVLGEF 2149
252 LQEQVQVEMMSKP 266

RESULT 14
2AAB_HUMAN STANDARD; PRT; 601 AA.
AC P40154; 075620;
DI 01 APR 1993 (rel. 25, created)
DI 15 JUL 1999 (rel. 48, last sequence update)
DI 01 OCT 2000 (rel. 40, last annotation update)
DE SEPRF/110F0F7NP PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A,
DE BETA ISOFORM (PP2A, SUBUNIT A, PP65-BETA ISOFORM) (PP2A, SUBUNIT A,
DE R1-BETA ISOFORM).
GN PP2R1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartidii; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 9014242; PubMed 9795170;
RA Baysal B.E., Farr J.E., Devlin B., Richard C.W., III;
RT "Genomic organization and precise physical location of protein
RT phosphatase 2A regulatory subunit A beta isoform gene on chromosome
RT band 11q23."
RL Gene 217:107-116(1998).
RN [2]
RP SEQUENCE OF 27-601 FROM N.A.
RX MEDLINE 90241887; PubMed 2159427;
RA Homnings B.A., Adams-Pearson C., Maurer F., Mueller P., Goris J.,
RA Mollath B., Hestermann S., Sten S.K.;
RT "Alpha- and beta-forms of the 65-kDa subunit of protein phosphatase
RT 2A have a similar amino acid repeating structure."
RL Biochemistry 29:3166-3173(1990).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT LUNG CANCER ASP-90.
RX MEDLINE 98438696; PubMed 9765152;
RA Wang S.S., Esplin E.D., Li J., Gazdar A., Minna J.,
RA Evans G.A.;
RT "Alterations of the PP2R1B gene in human lung and colon cancer."
RL Science 282:284-297(1998).

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EMBL: X73524; CAA51920.1;
InterPro: IPR001664;
Pfam: PF00038; Filament; 1.
PROSITE: PS00226; IF; 1.
Intermediate filament; Muscle protein.
INIT_MET 0
DOMAIN 1 107
DOMAIN 108 410
DOMAIN 411 468
DOMAIN 108 189
DOMAIN 146 149
DOMAIN 150 250
DOMAIN 251 266
DOMAIN 267 285
DOMAIN 286 293
DOMAIN 294 410
SEQUENCE 468 AA; 5365 MW; ED05667A5AE7FA8B CR64;

Query Match: 0.68; Score 70; DB 1; Length 468;
Best local similarity 29.38; Pred. No. 3.6;
Matches 22; Conservative 13; Mismatches 40; Gaps 0;

205 LNYQILKLEKESKPVFAALIVLALAKELFNYVLLFESTFELMELREVERHQ 214
192 LQREQLPEFAENNAAPFAVIAVLAIPPEPTESINETAFKVFHETRELOAQ 251
2125 QKTIQQLFIVLGEF 2149
252 LQEQVQVEMMSKP 266

RESULT 14
2AAB_HUMAN STANDARD; PRT; 601 AA.
AC P40154; 075620;
DI 01 APR 1993 (rel. 25, created)
DI 15 JUL 1999 (rel. 48, last sequence update)
DI 01 OCT 2000 (rel. 40, last annotation update)
DE SEPRF/110F0F7NP PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A,
DE BETA ISOFORM (PP2A, SUBUNIT A, PP65-BETA ISOFORM) (PP2A, SUBUNIT A,
DE R1-BETA ISOFORM).
GN PP2R1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartidii; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 9014242; PubMed 9795170;
RA Baysal B.E., Farr J.E., Devlin B., Richard C.W., III;
RT "Genomic organization and precise physical location of protein
RT phosphatase 2A regulatory subunit A beta isoform gene on chromosome
RT band 11q23."
RL Gene 217:107-116(1998).
RN [2]
RP SEQUENCE OF 27-601 FROM N.A.
RX MEDLINE 90241887; PubMed 2159427;
RA Homnings B.A., Adams-Pearson C., Maurer F., Mueller P., Goris J.,
RA Mollath B., Hestermann S., Sten S.K.;
RT "Alpha- and beta-forms of the 65-kDa subunit of protein phosphatase
RT 2A have a similar amino acid repeating structure."
RL Biochemistry 29:3166-3173(1990).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT LUNG CANCER ASP-90.
RX MEDLINE 98438696; PubMed 9765152;
RA Wang S.S., Esplin E.D., Li J., Gazdar A., Minna J.,
RA Evans G.A.;
RT "Alterations of the PP2R1B gene in human lung and colon cancer."
RL Science 282:284-297(1998).

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QY 1054 KQAMVILHLTL 1064
 DB 95 ADILKIFIAHL 105
 RESULT 27
 ID UL87_HCVMA STANDARD; PRT; 941 AA.
 AC P16740;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PROTEIN UL87.
 GR UL87.
 OS human cytomegalovirus (strain AD169).
 OC viruses, beta viruses, beta 1A stage, betaherpesviridae.
 OC betaherpesvirinae; cytomegaloviruses.
 OX NCBI_TaxID:10360;
 (1)
 RP SEQUENCE FROM N.A.
 KX MEDLINE:90293639; PubMed:216119;
 KX Chee M.S., Bankier A.T., Beck S., Binkley R., Brown C.M., Corney R.,
 EA Wiersele M., Wiersele M., Wiersele M., Wiersele M., Wiersele M.,
 EA Predigoe E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell R.G.;
 EA "Analysis of the protein-coding content of the sequence of human
 cytomegalovirus strain AD169."
 RT Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BURP1,
 CC HSV 6 958, HSV 1 24 AND HSV UL87.
 CC
 CC This SwissProt entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/annouce>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X17403; CAA35361.1;
 DR PTR: S09851; S09851.
 FT CARBOHYD 37 37 N LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 591 591 N LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 661 661 N LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 861 861 N LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 941 AA; 104803 MW; 4725FF3606A8A814 P0464;
 Query Match 0.6%; Score 65; DB 1; Length 941;
 Best Local Similarity 33.3%; Pred. No. 39;
 Matches 18; Conservative 17; Mismatches 45; Indels 0; Gaps 0;
 QY 203 PAFYVLEAGLEVLAFYAEFTIVEA:VAALVSEHRIIARILTYTGKGFSLQYPAATY 262
 DB 545 FAETVGSLSDEIAVNAENTNKNVNMKAALSTAAAGSLGVAPFLPKNTTFVYMKHFK 604
 QY 263 MLCQISVKVTMTFVNSL 282
 DB 605 EPACTVSTFVNSDAVYNSL 624
 RESULT 28
 ID EF3B_YEAST STANDARD; PRT; 1343 AA.
 AC P53978;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ELONGATION FACTOR 3B (EF 3B).
 GR YEF3B OR EF3B OR YHL014W OR R2846.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetina, Saccharomycetes;
 OC Saccharomycetales, Saccharomycetaceae, Saccharomycetes.
 OX NCBI_TaxID 4932;
 RP SEQUENCE FROM N.A.
 RA Andre B., Itaqei Housaini I., Urrestarazu L.A., Vissers S.;
 RC Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN
 PP CHARACTERIZATION
 RX MEDLINE:98205886; PubMed:9544245;
 RX Sarthy A.V., McGenieal T., Capobianco J.O., Schmidt M., Green S.R.,
 RA Moehle C.M., Goldman R.C.;
 RT "Identification and kinetic analysis of a functional homolog of
 RT elongation factor 3, YEF3 in Saccharomyces cerevisiae."
 RT Yeast 14:249-253(1998).
 RN
 PP CHARACTERIZATION
 PX MEDLINE:98451818; PubMed:9778296;
 PA Maurice T.C., Marucci C.P., Pannathar C.S., Rayn R.M., Watt G.A.,
 PA Paziss J.W.;
 RT "A highly conserved intraspecies homolog of the Saccharomyces
 RT cerevisiae elongation factor 3 encoded by the HEF3 gene."
 RT Yeast 14:1105-1113(1998).
 PL
 CC -1- FUNCTION: THE MAIN ROLE OF EF 3 MAY BE TO TRANSDUCE NUCLEOSIDE
 CC TRIPHOSPHATE ENERGY INTO MECHANICAL ENERGY FOR TRANSLATION
 CC DURING TRANSLATION. EF-3 STIMULATES EF 1 ALPHA DEPENDENT BINDING
 CC OF AMINOACYL-TENA TO THE P10SOMF. YEF3/HEF3 SEEMS TO BE
 CC EXPRESSED ONLY IN SPECIAL CONDITIONS; IT IS NOT REQUIRED FOR
 CC SURVIVAL.
 CC
 CC -1- PATHWAY: PROTEIN BIOSYNTHESIS.
 CC
 CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS). EF-3 SUBFAMILY.
 CC
 CC -1- SIMILARITY: CONTAINS 10 HEAT REPEATS.
 CC
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 CC
 CC EMBL: 771290; CAA95874.1;
 DR SGB: S0034959; YNL014W.
 DR InterPro: IPR001617;
 PFam: PF00005; ABC_tran; 2;
 PROSITE: PS00211; ABC_TRANSPORTER; 2;
 PP POSITIVE: PS00377; HEAT_REPEAT; 1
 KW Protein biosynthesis; Elongation factor; Repeat; ATP-binding;
 KW RNA-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT DOMAIN 9 322 HEAT REPEATS DOMAIN.
 FT REPEAT 434 607 DOMAIN 1.
 FT REPEAT 672 660 DOMAIN 11.
 FT NP_BIND 452 459 ATP (POTENTIAL).
 FT NP_BIND 700 707 ATP (POTENTIAL).
 FT DOMAIN 1008 1030 IYS-RICH (BASIC).
 SQ SEQUENCE 1043 AA; 115737 MW; 3E590EE579D88A8 CRC64;
 Query Match 0.6%; Score 65; DB 1; Length 1043;
 Best Local Similarity 33.3%; Pred. No. 44;
 Matches 17; Conservative 8; Mismatches 26; Indels 0; Gaps 0;
 QY 2079 KVPFAAIITVIAIAPKIKENYIVLIPESTPEIAFMENECPEVHQQKTI 2129
 DB 143 KEKVAVLEVISLVDAAKEQIALKMPLELIPVLSKSMWDTKKGVKEAATTTI 193
 RESULT 29
 ID PPOC_PICPR STANDARD; PRT; 1372 AA.
 AC Q92E20;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

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EMBL: M60462; AAA34105.1; -
 HSSP: P15737; IGHS.
 InterPro: IPR000490; -
 Pfam: PF00332; Glyco_hydro_17; 1.
 PROSITE: PS00587; GLYCOSYL_HYDROL_F17; 1.
 Hydrolase; Glycosidase; Multiene family.
 NON_TER 1
 ACT_SITE 196 196 NUCLEOPHILE (BY SIMILARITY).
 ACT_SITE 256 256 PROTON DONOR (BY SIMILARITY).
 SEQUENCE 275 AA; 36496 MW; 8F09B913A50C8F85 CDS4;
 Query Match 0.6%; Score 64; DB 1; Length 275;
 Best Local Similarity 31.6%; Pred No 12;
 Matches 13; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
 QY 1428 VLAAYGKDALEADTFWESVCFESVQHQSLSMNILOY 1469
 :||| 1 1111 3 3 3 3 1111 1 1 1 1
 DB 99 ILANTPPKDSIFEGFENSEINFLIQFLVGHNFLLANVVPY 1469
 RESULT 42
 ID E136_TUBAN; STANUARG; PKI; 343 AA.
 AC P23547;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM G19 PRECURSOR
 DE (EC 3.2.1.39) ((1-3)-BETA-GLUCAN ENDOHYDROLASE) ((1-3)-BETA-
 DE GLUCANASE) (BETA-1,3-ENDOGLUCANASE) (PR-2b) (PR-35).
 OS Nicotiana tabacum (Common tobacco).
 GN Glucanase; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 GN Magnoliopsida; eudicotyledons; core eudicots; Asteridiales; Rubiidae; I,
 GN Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID:4097;
 [1]
 SEQUENCE FROM N.A.
 STRAIN CV, SAMSON NN;
 MEDLINE 91062359, PMID 2347115,
 Linthorst B.J.M., Melchers L.S., Mayer A., van Roekel J.S.C.,
 Cornelissen B.J.C., Bol J.F.;
 "Analysis of gene families encoding acidic and basic
 beta-1,3-glucanases of tobacco."
 Proc. Natl. Acad. Sci. U.S.A. 87:8756-8760(1990).
 [2]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 STRAIN-CV, XANTINI NC; TISSUE leaf,
 Ward P.P., Payne G.R., Meyer M.B., Williams S.C., Pincher S.S.,
 Sharkey F.C., Cook T.L., Taylor H.T., Ashby P., Melis F.,
 Ryals J.A.;
 "Differential regulation of beta-1,3-glucanase messenger RNAs in
 response to pathogen infection."
 Plant Physiol. 96:300-307(1991).
 [3]
 SEQUENCE OF 39-115, 157-158, 251-276 AND 338-343.
 van den Buike M., Bauw G., Castresana G., van Montagu M.,
 Vandekeerekeve J.,
 "Characterization of vascular and extracellular beta(1,3)-glucanases
 of tobacco: evidence for a strictly compartmentalized plant defense
 system."
 Proc. Natl. Acad. Sci. U.S.A. 86:2673-2677(1989)
 CC 1-1- FUNCTION: IMPLICATED IN THE DEFENSE OF PLANTS AGAINST PATHOGENS.
 CC 1-1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
 CC IN 1,3-BETA-D-GLUCANS.
 CC 1-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC 1-1- INDUCTION: NOT FOUND IN HEALTHY TISSUES, BUT ACCUMULATES TO HIGH
 CC LEVELS IN THE EXTRACELLULAR COMPARTMENT OF LEAVES IN RESPONSE TO
 CC PATHOGEN INFECTION OR TREATMENT WITH SALICYLIC ACID.
 CC 1-1- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.

Query Match 0.6%; Score 64; DB 1; Length 343;
 Best Local Similarity 31.6%; Pred No 15;
 Matches 13; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
 QY 1428 VLAAYGKDALEADTFWESVCFESVQHQSLSMNILOY 1469
 :||| 1 1111 3 3 3 3 1111 1 1 1 1
 DB 167 ILANTPPKDSIFEGFENSEINFLIQFLVGHNFLLANVVPY 208
 RESULT 33
 YL37_CAREL
 ID YL37_CAREL; STANDAPP; PPT; 400 AA
 AC P34428;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOTHETICAL 45.5 KDA PROTEIN P44B9.7 IN CHROMOSOME III.
 GN P44B9.7.
 OS Caenorhabditis elegans
 GN Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 GN Rhabditidae; Rhabditinae; Caenorhabditis.
 NCBI_TaxID:6230;
 [1]
 SEQUENCE FROM N.A.
 STRAIN-BRISTOL N2;
 MEDLINE 94150718; PubMed=7406339;
 Wilson R., Ainscough R., Anderson K., Hayes C., Perks M.,
 Bonfield T., Burton I., Gammell M., Garsay T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Dutton R., Favello A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifkin L., Lloyd C., Saunders D., Shownkeen R.,
 Sims M., Smeadon N., Smith A., Smith M., Sonhammer E., Staden R.,
 Sulston J., Thierry-Mieg J., Thomas K., Vardan M., Vaughan K.,
 Waterson P., Watson A., Weinstein L., Wilkinson-Sproat J.,
 Weidman P.;
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 Nature 368:33-38(1994).

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DR EMBL: K00922; AAA37104.1; JOINED.
DR EMBL: K00923; AAA37104.1; JOINED.
DR EMBL: K00924; AAA37104.1; JOINED.
DR EMBL: K00925; AAA37104.1; JOINED.
DR EMBL: K00926; AAA37104.1; JOINED.
DR PIR: A02959; VHY.
DR HSSP: P03069; LSWI.
DR InterPro: IPR001684; -.
DR Pfam: PF00038; Filament; 1.
DR PROSITE: PS00226; IF; 1.
DR KW Intermediate filament; Coiled coil; Heptad repeat pattern;
KW Acetylation; Phosphorylation.
FT INIT_MET 0 0
FT DOMAIN 1 93 HEAD.
FT DOMAIN 94 405 ROD.
FT DOMAIN 406 464 TAIL.
FT DOMAIN 94 129 COIL 1A.
FT DOMAIN 130 151 LINKER 1.
FT DOMAIN 152 243 COIL 1B.
FT DOMAIN 244 266 LINKER 12.
FT DOMAIN 267 405 COIL 2.
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 38 38 PHOSPHORYLATION (BY CAM-KINASE II)
FT MOD_RES 81 81 PHOSPHORYLATION (BY CAM-KINASE II)
FT MOD_RES 81 81 PHOSPHORYLATION (BY CAM-KINASE II)
FT CONFLICT 42 42 L -> A (IN REF. 2).
FT CONFLICT 115 115 Y -> D (IN REF. 2).
FT CONFLICT 162 162 R -> I (IN REF. 2).
SQ SEQUENCE 464 AA; 53598 MW; 7AC417008CB04776 CRC64;

Query Match 0.6%; Score 64; DB 1; Length 464;
Best Local Similarity 25.3%; Pred. No. 22;
Matches 20; Conservative 18; Mismatches 41; Indels 6; Gaps 0;

QY 2061 LMKPLRFLRLLETSKPKFAALITVALAPTKRNYVLIINSLPLAPLMPPPE 2129
DB 183 LREKLEEMIGREAEATLQSFQDVONASLAPLCPPEVSLQELAPLPLPHNRIQF 242

QY 2121 VEHCCTQTCQETVLAF 2139
DB 243 LQAQIQPHVQIDVDVSKP 261

RESULT 36
VIM_HUMAN STANDARD: PRT; 465 AA.
AC P08670;
DI 01-JAN-1988 (Rel. 06, Created)
DI 01-OCT-1993 (Rel. 27, Last sequence update)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DE VIMENTIN.
GN VIM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87089701; PubMed-3467175;
RA Ferrari S., Battini B., Kaczmarek L., Pittling S., Calabretta R.,
RA de Riel J.K., Philipidis V., Wei J., Basvetga R.,
PT "Cloning sequence and growth regulation of the human vimentin gene".
Mol. Cell. Biol. 6:3614-3620(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91067467; PubMed-2251132;
RA Honore B., Madsen P., Basse R., Andersen A., Walbum E., Gellis J.E.,
RA Letters H.;
PT "Nucleotide sequence of cDNA covering the complete coding part of the
human vimentin gene".
Nucleic Acids Res 18:6692-6692(1990).


```

RX MEDLINE: 9217196; PubMed:1540169;
RA Busomakers M.J.G., Verhaegh G.W.C. et al. 1990. Bacterium A.
RA Debruyne P.M.J., Schaiken J.A.
RA "Differential expression of vimentin in rat prostatic tumors."
RL Biochem. Biophys. Res. Commun. 182:1254-1259(1992).
RN 121
RP SEQUENCE OF 85 159 FROM N.A.
RA Paine M.L.
RA Submitted (XXX-1992) to the EMBL/GenBank/DBP databases.
CC -1- FUNCTION: VIMENTIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN
CC VARIOUS NONEPITHELIAL CELLS, ESPECIALLY MESENCHYMAL CELLS.
CC -1- SUBUNIT: HOMOPOLYMER.
CC -1- PTM: ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS OF
CC MESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL
CC DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
CC REORGANIZED.
CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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CC
CC EMBL: X62952; CAA44722.1; -
CC EMBL: M84481; AAA42339.1; -
CC FIC: S22119; S22119.
CC FIC: JQ1389; JQ1389.
CC HSP: P03659; ISW1.
CC InterPro: IPR001664; -
CC Pfam: PF00038; filament; 1.
CC PROSITE: PS00236; IF; 1.
CC
CC KW Intermediate filament; Coiled coil; Heptad repeat pattern;
CC Phosphorylation.
CC
CC INIT_MET 0 0 BY SIMILARITY.
CC FT DOMAIN 1 94 HEAD.
CC FT DOMAIN 95 406 ROD.
CC FT DOMAIN 407 465 TAIL.
CC FT DOMAIN 95 130 COIL 1A.
CC FT DOMAIN 131 152 LINKER 1.
CC FT DOMAIN 153 244 COIL 1B.
CC FT DOMAIN 245 267 LINKER 12.
CC FT DOMAIN 268 406 COIL 2.
CC FT MET_RES 38 38
CC
CC MISC_NIS 82 82
CC FT PHOSPHORYLATION (BY CAM-KINASE II)
CC FT PHOSPHORYLATION (BY CAM-KINASE II)
CC FT (BY SIMILARITY).
CC FT (BY SIMILARITY).
CC SEQUENCE 465 AA; 53601 MW; 6587E7652CB5682 CRC64;

Query Match 0.6%, Score 64; DB 1; Length 465;
Best Local Similarity 25.3%, Pred. No. 22;
Matches 20, Conservative 18; Mismatches 41; Indels 0; Gaps 0;

QY 2061 LWKPLRVLLKLTSSSTKRVNALTVLAAELKERNVIVLLFESIFLAELMEDECEP 2129
DB 184 LREKLQEMQLQREAEASTLQSFQVDNANLALDLERKVESTLQETAPLKKKHDFEIQE 243

QY 2121 VRRGCKTQQEETVIGEP 2129
DB 244 LQAOIQHQVQIDVDVSKP 252

RESULT 39
DNAB: BACME
ID DNAB: BACME STANDARD; PPT: 605 AA.
AC P05646;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNAB PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70).

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GN DNAB.
OS Bacillus megaterium
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus
CC NCRI_TaxID=1404;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE:87231083; PubMed:3035506;
RA Sussman M.D., Setlow P.
RA "Nucleotide sequence of a Bacillus megaterium gene homologous to the
RA dnaK gene of Escherichia coli."
RL Nucleic Acids Res. 15:3923-3923(1987).
CC -1- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC
CC EMBL: Y00154; CAA68348.1; -
CC HSP: P04475; 1DKX.
CC InterPro: IPR001023; -
CC Pfam: PF00012; HSP70; 1
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70.1; 1
CC PROSITE: PS00329; HSP70.2; 1.
CC PROSITE: PS01036; HSP70.3; 1.
CC
CC KW Chaperone; ATP-binding; Heat shock.
CC SEQUENCE 605 AA; 65250 MW; 1CBCC2C4F34A9334 CRC64;

Query Match 0.6%, Score 64; DB 1; Length 605;
Best Local Similarity 32.7%, Pred. No. 31;
Matches 17, Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 548 FSEVTSINLLNFQRAELSKNGEWELVIAADILIKEITLSENDQLSNV 599
DB 514 FTEKTKIKDIEGKVEAEVTKANFAKDAKAAATKKNDELETKAKKDELEIV 565

RESULT 40
Y228_BORBU
ID Y228_BORBU STANDARD; PPT: 471 AA
AC O51246;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYDROTHERMAL PROTEIN BR0228.
GN BR0228
OS Borrelia burgdorferi ( Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
CC NCRITaxID=139;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE:ATCC 35210 / B31;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey P.K., Swinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Petersen J., Karpavay A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt P., Palmer N., Adams M.D., Corayne J.D., Weidman J.,
RA Utterback T., Watthey L., McDonald L., Artach P., Howman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.
RA "Genomic sequence of a Lyme disease spirochete, Borrelia
RA burgdorferi."
PL Nature 390:580-586(1997).

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Best Local Similarity 28.6%, Pred. No. 28;
Matches 14; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

DR 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
KW 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
FT 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
SQ 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355

DR 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
KW 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
FT 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
SQ 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235

Query Match 0.6%; Score 61; DB 1; Length 270;
Best Local Similarity 35.3%; Pred. No. 29;
Matches 12; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

DR 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
KW 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
FT 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
SQ 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780

DR 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
KW 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
FT 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
SQ 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258

RESULT 62
ID CTR3-CHICK STANDARD; PRT: 456 AA.
AC P28568;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCOSE TRANSPORTER TYPE 3 (CEP-GR3).
GN SLC2A3 OP GLUT3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=91342646; PubMed=1875942;
RA White M.K., Fall T.R., Weber M.J.;
RT "Differential regulation of glucose transporter isoforms by the src
oncogene in chicken embryo fibroblasts";
RL Mol. Cell. Biol. 11:4448-4454(1991).
CC -1- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEURONAL
GLUCOSE TRANSPORTER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: HIGH TO OTHER GLUCOSE TRANSPORTERS.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC
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EMBL: M37785; AAA8662.1;
PIR: A41264; A41264.
TranPro: IPR000803;
InterPro: IPR001066;
InterPro: IPR002945;
Pfam: PF00083; Sugar tr. 1;
PRINTS: PR00171; SUGTRNSPORT.
DR PRINTS: PR00172; GLUCTRNSPORT.
DR PRINTS: PR01192; GLUCTRNSPORT3.
DR PROSITE: PS00216; SUGAP_TRANSPORT_1; 1.
DR PROSITE: PS00217; SUGAP_TRANSPORT_2; 1.
CC Duplication; Transmembrane; Sugar transport; Transport; Glycoprotein;
KW Multigene family.
FT TRANSMEM 12 32
FT DOMAIN 33 65
FT TRANSMEM 66 86
FT TRANSMEM 95 115
FT TRANSMEM 126 146
FT TRANSMEM 155 175
FT TRANSMEM 185 205
FT DOMAIN 206 270
FT TRANSMEM 271 291

Best Local Similarity 28.6%, Pred. No. 28;
Matches 14; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

DR 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
KW 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
FT 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355
SQ 1407 LAGTAVGIPPPKVLNIMSTFEMGANVMMIDITYSGVINKTVRMVTP 1355

DR 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
KW 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
FT 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235
SQ 187 LNCIVASLIPTPCHPFLMSTYSFSGENFQAKTVKTTVLDMWPELQ 235

Query Match 0.6%; Score 61; DB 1; Length 270;
Best Local Similarity 35.3%; Pred. No. 29;
Matches 12; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

DR 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
KW 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
FT 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780
SQ 1747 TSELVSSEVYLLSAAIAAKVVFTHPHFTSPYLF 1780

DR 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
KW 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
FT 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258
SQ 225 TDDLLPHPYIAERLFVLESLOEIAPIHPILK 258

RESULT 61
ID SULD-STERN STANDARD; PRT: 270 AA.
AC P22294; 044697;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FUNCTIONAL FOLATE SYNTHESIS PROTEIN [INCLUDES: DIHYDROFOLATE
ALDOSE (OC 4.1.2.25) (DHNA); 2-AMINO-4-HYDROXY-6-
HYDROXYMETHYLDIHYDROFOLATE LINE PYROPHOSPHOKINASE (EC 2.7.6.3) (7.8-
DIHYDRO-6-HYDROXYMETHYLTERIN PYROPHOSPHOKINASE) (HPPK) (6-
HYDROXYMETHYL-7,8-DIHYDROFOLATE IN PYROPHOSPHOKINASE) (PPPK)].
GN SULD.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacilli; Fusobacteriium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
PP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13.
PP STRAIN 708;
PP MEDLINE=90368525; PubMed=2168467;
PP Lopez P., Greenberg B., Lacks S.A.;
PP "cDNA sequence of folate biosynthesis gene suld, encoding
hydroxymethyldihydrofolate pyrophosphokinase in Streptococcus
pneumoniae, and characterization of the enzyme";
PP J. Bacteriol. 172:4766-4774(1990).
RN [2]
PP REVISIONS TO 156-170.
PP STRAIN 772;
PP MEDLINE=95095988; PubMed=7798151;
PP Lacks S.A., Greenberg B., Lopez P.;
PP "A cluster of four genes encoding enzymes for five steps in the
folate biosynthetic pathway of Streptococcus pneumoniae";
PP J. Bacteriol. 177:66-74(1995).
RN [3]
PP CHARACTERIZATION.
PP MEDLINE=93244440; PubMed=838566;
PP Lopez P., Lacks S.A.;
PP "A bifunctional protein in the folate biosynthetic pathway of
Streptococcus pneumoniae with dihydropteridin aldolase and
hydroxymethyldihydropteridin pyrophosphokinase activities";
PP J. Bacteriol. 175:2214-2220(1993).
CC -1- CATALYTIC ACTIVITY: 2-AMINO-4-HYDROXY-6-(D-EPYTHRO-1,2,3-
TRIHYDROXYMETHYL) 7,8-DIHYDROFOLATE + 2-AMINO-4-HYDROXY-6-
HYDROXYMETHYL-7,8-DIHYDROFOLATE + 2-AMINO-4-HYDROXY-6-
DIHYDROFOLATE + AMP + 2-AMINO-7,8-DIHYDRO-4-HYDROXY-6-
(DIHYDROXYMETHYL)PTERIDINE.
CC -1- PATHWAY: FOLATE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTRIMER OR HOMOTETRAMER.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE DHNA FAMILY
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE HPPK FAMILY.
CC
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EMBL: U16156; AAB63947.1;
PIR: A36704; A36704.
InterPro: IPR000550;
Pfam: PF01288; HPPK; 1.

XX MEDLINE-91342636; PubMed-1875927;
 VA Lock P., Ralph S., Stanley E., Boulet J., Ramsay P., Dunn A.P.;
 AT "Two isoforms of marine hck, generated by utilization of alternative
 AT translational initiation codons, exhibit different patterns of
 AT subcellular localization.";
 AT Mol. Cell. Biol. 11:4363-4370(1991).
 AT [4]
 AT X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 AT MEDLINE-97177106; PubMed-9024658;
 AT Sichari F., Moarefi I., Kuriyan J.;
 AT "Crystal structure of the Src family tyrosine kinase Hck.";
 AT Nature 385:602-609(1997).
 AT [5]
 AT STRUCTURE BY NMR OF 78-138.
 AT MEDLINE-96239731; PubMed-9571048;
 AT Horita D.A., Baldissari D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 AT Gmeliner W.H., Byrd R.A.;
 AT "Solution structure of the human Hck SH3 domain and identification of
 AT its ligand binding site.";
 AT J. Mol. Biol. 278:253-265(1998).
 AT [6]
 AT STRUCTURE BY NMR OF 139-245.
 AT MEDLINE-97253487; PubMed-9109402;
 AT Zhang W., Smithgall T.E., Gmeliner W.H.;
 AT "Sequential assignment and secondary structure determination for the
 AT Src homology 2 domain of hematopoietic cellular kinase";
 AT FEBS Lett. 406:141-145(1997).
 AT [7]
 AT X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 AT MEDLINE-98453315; PubMed-9778343;
 AT Arnold S., O'Brien P., Franken P., Strub M.P., Hoh P., Dumas C.,
 AT Ladbury J.R.;
 AT "RT loop flexibility enhances the specificity of Src family SH3
 AT domains for HIV-1 Nef.";
 AT Biochemistry 37:14683-14691(1998).
 AT [8]
 AT FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE EC
 AT RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST MAY ALSO
 AT CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 AT DEGRANULATION PROCESS OF NEUTROPHILS.
 AT CATALYTIC ACTIVITY: ATP -> A PROTEIN TYROSINE - ADP +
 AT PROTEIN TYROSINE PHOSPHATE.
 AT [9]
 AT SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH
 AT MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 AT [10]
 AT ALTERNATIVE PRODUCTS: THE P60-HCK AND P59-HCK ARE PRODUCED BY THE
 AT USE OF ALTERNATIVE INITIATION SITES.
 AT [11]
 AT TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 AT MYELOID AND B LYMPHOID LINEAGES.
 AT [12]
 AT SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 AT [13]
 AT SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
 AT DOMAIN. BELONGS TO THE SRC SUBFAMILY.
 AT
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 AT or send an email to license@isb-sib.ch).
 AT
 AT EMBL: M16591; AAA52643.1; -;
 AT EMBL: M16592; AAA52644.1; -;
 AT EMBL: A27812; TVH0HC.
 AT PIR: 2HCX; 20-APR-97.
 AT PIR: 3HCX; 15-OCT-97.
 AT PIR: 4HCX; 17-JUN-98.
 AT PIR: 5HCX; 17-JUN-98.
 AT PIR: 1AD5; 15-MAY-97.
 AT PIR: 1B01; 11-NOV-98.
 AT MIM: 142370; -;
 AT InterPro: IPR000719; -;
 AT InterPro: IPR000980; -;
 AT InterPro: IPR001245; -;

DR InterPro: IPR001452; -;
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR PRINTS: PF06104; TYRKINASE.
 DR PRINTS: PF06401; SH3DOMAIN.
 DR PRINTS: PF00452; SH3DOMAIN.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50003; Tyrosine protein kinase; Phosphorylation; AIP-binding;
 DR Myristate; SH2 domain; SH3 domain; Alternative initiation;
 KW 3D-structure.
 KW CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.
 KW CHAIN 2 526 TYROSINE-PROTEIN KINASE P59-HCK.
 KW INIT_MET 22 22 POP P59-HCK.
 KW LIPID 2 2 MYRISTATE (BY SIMILARITY).
 KW LIPID 23 23 MYRISTATE (BY SIMILARITY).
 KW DOMAIN 78 138 SH2.
 KW DOMAIN 144 241 SH2.
 KW DOMAIN 262 515 PROTEIN KINASE.
 KW NP_BIND 288 276 ATP.
 KW BINDING 290 290 ATP.
 KW ACT_SITE 381 381 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 KW MOD_RES 411 411 S -> C (IN AAA52644).
 KW CONFLICT 24 24 S -> C (IN AAA52644).
 KW SEQUENCE 526 AA; 59583 MW; 347E877A0A6412B3 CRC64;
 SQ
 Query Match 0.68; Score 61; DB 1. Length 526;
 Best Local Similarity 21.7%; Pred. No. 65;
 Matches 10; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1210 ILELQHKKLRSPQIIVPTLFLNLSNCTEPHPOGNGMYETKGLI 1255
 DB 466 VIRALRGYRPRPCPEDELYNIMMKCKMKPKPKETFEYIGSVL 511
 RESULT 65
 ID BYR2_SCHPO STANDARD; FRK; 659 AA.
 AC P28829;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROTEIN KINASE BYR2 (EC 2.7.1.1) (PROTEIN KINASE SH2) (MAPE KINASE
 DE KINASE) (MAPKK).
 DE BYR2 OR STE8 OR SPRC1D7.05.
 DE Schizosaccharomyces pombe (Fission yeast).
 DE Eukaryota, Fungi; Ascomycota; Schizosaccharomycetes;
 DE Schizosaccharomycetales; Schizosaccharomycetaceae;
 DE Schizosaccharomyces.
 DE NCBI_TaxID=4896;
 DE [1]
 DE SEQUENCE FROM N.A.
 DE MEDLINE-91260705; PubMed-2846669;
 DE Wang Y., Xu H.P., Rigas M., Rodgers L., Wigler M.;
 DE "byr2, a Schizosaccharomyces pombe gene encoding a protein kinase
 DE capable of partial suppression of the ras1 mutant phenotype.";
 DE Mol. Cell. Biol. 11:3554-3563(1991).
 DE [2]
 DE SEQUENCE FROM N.A.
 DE MEDLINE-95062795; PubMed-1435723.
 DE Stykarsdottir O., Egel R., Nielsen O.;
 DE "Functional conservation between Schizosaccharomyces pombe ste8 and
 DE saccharomyces cerevisiae Ste11 protein kinases in yeast signal
 DE transduction.";
 DE Mol. Gen. Genet. 235:122-130(1992).
 DE [3]
 DE SEQUENCE FROM N.A.
 DE RP STRAIN-972;

BA Wood V., Rajanahram M.A., Bartell R.C., Skolton J., Chutcher C.M.;
 Submitted (Aug 1997) to the EMBL/GenBank/Trna databases
 CC 1- FUNCTION: SUBSTITUTED ADENYLATE-DEPENDENT KINASE INVOLVED IN CARRIAGE
 CC AND STORAGE. IT IS THOUGHT THAT IT PHOSPHORYLATES THE MYRI
 CC PROTEIN KINASE WHICH ITSELF PHOSPHORYLATES THE SERI KINASE.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE KINASE SUBFAMILY
 CC 1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC
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EMBL: M74273; AAA5289.1
 DB EMBL: X00851; CAA4874.1
 DB EMBL: Z98799; CAA1061.1
 DB PIR: A3728; A36724
 DB PIR: S3094; S3094
 DB RSCD: Q60450; IABG
 DB InterPro: IPR000196
 DB InterPro: IPR000196
 DB InterPro: IPR000196
 DB Pfam: Pfam068; SAM_1
 DB Pfam: Pfam068; SAM_1
 DB ProSITE: PS00107; PROTEIN KINASE_ATP_1
 DB ProSITE: PS00106; PROTEIN KINASE_S1_1
 DB ProSITE: PS00110; PROTEIN KINASE_TPM_1
 KW Translocase, Serine/threonine-protein kinase, ATP binding,
 KW Serine/threonine-specific protein kinase
 FT DOMAIN 494 658 PROTEIN KINASE
 FT NP_BIND 400 498 ATP (BY SIMILARITY)
 FT BINDING 424 424 ATP (BY SIMILARITY)
 FT ACT_SITE 522 522 HY SIMILARITY
 SEQUENCE 659 AA; 7.66 kDa; MW: 160706110; PABRD CRG64;

Query Match 0.68; Score 61; Db 1; Length 659;
 Best Local Similarity 31.78; Prod. No. 97;
 Matches 13; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

CV 1579 ALKRAYLILKVKALILKILKIPVIRIVNIPVSVKRALINKKL 1627
 DB 170 AALSSSLSPKLVVGLVLRKRVKRNARTNYVFFVLRKEL 218

RESULT 16
 PROX1 HUMAN
 ID PROX1 HUMAN STANDARD; PRI: 735 AA.
 AC 292796
 DT 15-JUL-1998 (Rel. 47, Last sequence update)
 DI 15-JUL-1998 (Rel. 47, Last sequence update)
 DE HOMEOBOX PROSPEPO LIKE PROTEIN PROX1 (PROX1).
 GN PROX1
 OS Homo sapiens (Human)
 SW Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi:
 SW Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
 RX NBI_104106
 SEQUENCE FROM N.A.
 MEDLINE 9601156; PubMed 9612456
 Zingales A.P., Hansen M.F., Adams G.L., Fries R.,
 Polymeropoulos M.H., Tomarow S.L.;
 "Structure and chromosomal localization of the human homeobox gene
 PROX1";
 Genomics 45:517-522(1996).
 1 FUNCTION: MAY PLAY A TUMOR-SUPPRESSOR ROLE IN EARLY DEVELOPMENT OF CNS.
 MAY REGULATE GENE EXPRESSION AND DEVELOPMENT OF POSTMITOTIC

CC UNDIFFERENTIATED YOUNG NEURONS (BY SIMILARITY).
 CC 1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC 1- TISSUE SPECIFICITY: MOST ACTIVELY EXPRESSED IN THE HYPOTHALAMUS,
 CC LENS, DETECTED ALSO IN EMBRYONIC BRAIN, LUNG, LIVER, AND KIDNEY.
 CC IN ADULT, IT IS MORE ABUNDANT IN HEART AND LIVER THAN IN BRAIN,
 CC SKELETAL MUSCLE, KIDNEY, AND PANCREAS.
 CC 1- SIMILARITY: BELONGS TO THE PROSPEPO FAMILY OF HOMEOBOX PROTEINS.
 CC
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 CC or send an email to: license@ebi.ac.uk).

EMBL: U44060; AAC50656.1
 DB EMBL: 601546
 DB EMBL: 601546
 KW Homeobox; DNA-binding; Nuclear protein; Transcription regulation;
 KW Developmental protein.
 FT DOMAIN 215 219 POLY-GLN
 FT DNA_BIND 572 634 HOMEOBOX (ATYPICAL)
 FT DOMAIN 635 736 PROSPEPO-LIKE
 SEQUENCE 736 AA; 83162 MW; 8EC94BEBA0E7A18 CRG64;

Query Match 0.68; Score 61; Db 1; Length 736;
 Best Local Similarity 31.78; Prod. No. 97;
 Matches 13; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

CV 1472 KATPEEFILKRAVSESESEPEFEMVIVNIESEKQHR 1512
 DB 212 FVSSVSESLSPKLVVGLVLRKRVKRNARTNYVFFVLRKEL 218

RESULT 67
 V14_ROTTP
 ID V14_ROTTP STANDARD; PRI: 775 AA.
 AC 011195;
 DT 01-JUL-1989 (Rel. 11, Created)
 DI 01-NOV-1990 (Rel. 16, Last sequence update)
 DI 01-APR-1993 (Rel. 25, Last annotation update)
 DE OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OTHER LAYER PROTEIN VP4)
 DE [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP6].
 GN S4
 OS Human rotavirus (serotype 3 / strain P).
 SW Viruses: Gsera viruses, Rotviridae, Rotavirus.
 CX NCBI_104106; 10957;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 88275070; PubMed 2849714;
 RA Gorzilia M., Chanock R.M., Nishigaki Y., Lestipedi K., Jones R.,
 RA Kapihan A.Z., Chanock R.M.;
 RT "Sequence of the fourth gene of human rotaviruses recovered from
 RT asymptomatic or symptomatic infections."
 RL J. Virol. 62:2978-2984(1988).
 RN 121
 RP SEQUENCE OF 1-280
 RX MEDLINE 86413706; PubMed 9018754;
 RA Gorzilia M., Hoshino Y., Buckler-White A., Humentals L., Glass R.,
 RA Flores J., Kapihan A.Z., Chanock R.M.;
 RT "Characterization of amino acid sequence of VP6 and cleavage region of
 RT 84-kDa outer capsid protein among rotaviruses recovered from
 RT asymptomatic neonatal infection."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7039-7043(1988).
 CC 1- SUBCELLULAR LOCATION: OUTER CAPSID.
 CC 1- PTM: VP6 IS ONE OF TWO PEPTIDES CLEAVAGE PRODUCTS OF VP4; THE
 CC OTHER PRODUCT IS VP5.
 CC 1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
 DB PIR: C28839; V14RW5.
 DB PIR: R25904; V14RPP.
 DB InterPro: IPR000416;
 DB Pfam: Pfam0426; VP4_1.

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 CC or send an email to license@sib-sb.ch).

CC EMBL: X03841; CAA27446.1; -
 CC DR PIR: A23386; SAZGGM.
 CC DR InterPro: IPR000561; -
 CC DR Pfam: PF00008; EGF; 1.
 CC DR Malaria: Merzoite; Polypeptide; Repeat; Signal; Glycoprotein;
 CC Transmembrane; GPI-anchor.
 CC KW SIGNAL: 1 19 POTENTIAL.
 CC FT CHAIN: 20 1726 MERZOITE SURFACE PROTEIN 1
 CC FT CARBOHYD: 133 133 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 272 272 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 501 501 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 567 567 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 638 638 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 827 827 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 924 924 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 990 990 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1016 1016 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1114 1114 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1221 1221 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1613 1613 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1726 1726 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 1726 AA; 196197 MW; 509A545FA352BCF3 CRC64;

CC Query Match: 0.6%; Score 61; DR 1; Length 1726;
 CC Best Local Similarity: 30.2%; Prod. No. 2.7e+03;
 CC Matches: 16; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

CC 968 SDAAYVIGDIALFEELQKKIKSKHKLSETLKLSCVSYSTSYAKDLMK 1020
 CC 1 1111 1111 1111 1111
 CC 1408 SSNEYIIEESFKLNSQKNTLLSKYKIVKESVNDIKFAGEGISYVEKVIK 1460

CC RESULT 76
 CC MSPI_PLAAPP STANDARD: PRT: 1726 AA.
 CC ID MSPI_PLAAPP AC P50495;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
 CC DE MERZOITE SURFACE PROTEIN 1: PEPPIPS-4 (MERZOITE SURFACE ANTIGENS)
 CC DE (PMMSA) (Q195).
 CC CN MSP-1.
 CC OS Plasmodium falciparum (isolate Palo Alto / Uganda).
 CC OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC OX NML_TaxID-57270;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RP MEDLINE-B5005525; PubMed-3049134.
 CC RA Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.P.,
 CC KA Siddiqui W.A.;
 CC "Plasmodium falciparum: gene structure and hydrophobic profile of the
 CC major merozoite surface antigen (gp195) of the Uganda-Palo Alto
 CC isolate.";
 CC RT EXP. Parasitol. 67:1-11(1988).
 CC CC
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 CC (POTENTIAL).
 CC -1- PTM: MERZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42
 CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
 CC MERZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT
 CC
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CC EMBL: M37213; AAA29611.1; -
 CC DR InterPro: IPR000561; -
 CC DR Pfam: PF00008; EGF; 1.
 CC DR Malaria: Merzoite; Polypeptide; Repeat; Signal; Glycoprotein;
 CC Transmembrane; GPI-anchor.
 CC KW SIGNAL: 1 19 POTENTIAL.
 CC FT CHAIN: 20 1726 MERZOITE SURFACE PROTEIN 1
 CC FT CARBOHYD: 133 133 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 272 272 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 501 501 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 567 567 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 638 638 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 827 827 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 924 924 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 990 990 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1016 1016 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1114 1114 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1221 1221 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1613 1613 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD: 1726 1726 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 1726 AA; 196174 MW; 5B59CELEFA19A026 CRC64;

CC Query Match: 0.6%; Score 61; DR 1; Length 1726;
 CC Best Local Similarity: 30.2%; Prod. No. 2.7e+03;
 CC Matches: 16; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

CC 968 SDAAYVIGDIALFEELQKKIKSKHKLSETLKLSCVSYSTSYAKDLMK 1020
 CC 1 1111 1111 1111 1111
 CC 1408 SSNEYIIEESFKLNSQKNTLLSKYKIVKESVNDIKFAGEGISYVEKVIK 1460

CC RESULT 77
 CC TRX_DROVI STANDARD: PRT: 3828 AA.
 CC ID TRX_DROVI AC Q24742;
 CC DT 01-OCT-2000 (Rel. 40, Created)
 CC DT 01-OCT-2000 (Rel. 40, Last sequence update)
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
 CC DE TRITHORAX PROTEIN.
 CC GN TRX.
 CC OS Drosophila virilis (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC OC Ephydrozoa; Prosoptilidae; Trosophilla
 CC OX NCHI_TaxID-7244;
 CC RN [1]
 CC PP SEQUENCE FROM N.A.
 CC MEDLINE-B6100387; PubMed-8555104;
 CC RA Tillib S., Sedkov Y., Mizrokhi L., Mazo A.;
 CC "Conservation of structure and expression of the trithorax gene
 CC between Drosophila virilis and Drosophila melanogaster.";
 CC Mech. Dev. 53:113-122(1995).
 CC -1- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION
 CC WITH GENES OF TRITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.
 CC IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FING ZINC-FINGER DOMAINS.

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EMBL: M35861; AAA34413.1; -
EMBL: M17133; AAA35182.1; -
EMBL: X16765; CAA34411.1; ALU_INT1.
EMBL: X59720; CAA3259.1; -
PIR: A36362; A36362.
PIR: JN0133; JN0133.
PIR: S11169; S11169.
PIR: S19499; S19499.
SGD: S0000680; TUP1.
InterPro: IPR001680; -
Pfam: PF00400; WD40; 7.
PRINTS: P00320; GPROTEINREPT.
PROSITE: PS00676; WD_REPEATS_1; 4.
PROSITE: PS50082; WD_REPEATS_2; 5.
PROSITE: PS50294; WD_REPEATS_REGION; 1.
Transcription regulation: Repressor; Repeat, WD repeat.
REPEAT 342 371 WD 1.
REPEAT 441 471 WD 2.
REPEAT 483 513 WD 3.
REPEAT 524 555 WD 4.
REPEAT 574 604 WD 5.
REPEAT 628 658 WD 6.
REPEAT 670 706 WD 7.
DOMAIN 97 118 POLY-GLN.
DOMAIN 181 198 POLY-GLN.
DOMAIN 399 409 THR-RICH.
CONFLICT 75 75 E -> A (IN REF. 1).
CONFLICT 100 100 R -> Q (IN REF. 1).
CONFLICT 685 685 P -> S (IN REF. 1 AND 2).
SEQUENCE 713 AA; 78307 MW; 444104AA063CB944 CRC64;

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Very Match	0.68	Score 60	DB 1	Length 713
1st Local Similarity	35.0%	Pred. No. 1.3e+02		
14. Conservative	10	Mismatches 16	Indels 0	Gaps 0

1159 EGVRIELEIPDKAKPIGTVGQFPQMCKKSKCHISVGE 1198
:
:
:
78 FHLKLTNFGPDGTAFTWGGAPCGCCGAGVGHILQQQQO 117

BL 94
ROTHD -
VP4_ROTHD STANDARD; PKT; 775 AA.
P11196;
01-JUL-1989 (Rel. 11, Created)
01-NOV-1990 (Rel. 16, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP81.

MEDLINE-86313706; PubMed=3018754;
Garcia-Jim M., Hsueh Y., Becker White A., Ruppertsals I., Glass P., Flores J., Kapikian A.Z., Chanock R.M.;
"Conservation of amino acid sequence of VP8 and cleavage region of HA-2 outer capsid protein among rotaviruses recovered from asymptomatic neonatal infection,"
Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043 (1986).
-1- SUBCELLULAR LOCATION: OUTER CAPSID.
-1- PPM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE OTHER PRODUCT IS VP5.
-1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.

every Match	0.6%	Score 60;	DB 1;	Length 775;
1st Local Similarity	55.6%	Fred. No. 1.4e+02;		
16; Conservative		8; Mismatches	21; Indels	0; Gaps

```

1045 IQKPTAVILKQDAWVLHLTLCKYNEFSVSLNEDPKSLDIFIKAV 1089
      ||||| :: | || : | ||| : | :: | : |
657 LKPSRVVLKIDVEVMEINTEGKFAYRKVDLTLINEFFDNKFAELV 711

```


01 JUN-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL I13.7 KDA PROTEIN C14B9_6 IN CHROMOSOME III,
C14B9_6.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough K., Anderson K., Haynes C., Belks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin P., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins L., Hillier L., Jier M.,
Johnston L., Jones M., Ker Shaw J., Kirsten J., Laissner N.,
Latreille P., Lightfoot J., Lloyd C., Mortimore B., O'Callaghan M., Pat
Parsons T., Perry G., Pfaffenberger A., Saunders D., Showkeen R.,
Sims M., Smalton N., Smith A., Smith K., Sonnhammer E., Staden R.,
Stultgen J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson P., Watson A., Weinstein L., Wilkinson-Sproat J.,
Wohlman P.;
#2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.*;
Nature 368:32-38(1994).

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EMBL: LJ5188; AAA27950.1; -
PIP; S44758; S44758.
Uniprot: C14B9_6; P600077
InterPro: IPRO01005; -
Pfam: PF00249; myb_DNA-binding; 1.
PSORT: ps00090; MYB_3; 1.
KW Hypothetical protein.
SEQUENCE 1018 AA; 11490 MW; 94/5A1765216E3F CRG64;
Query Match 0 %; Score 60; DB 1; Length 1018;
Best Local Similarity 26.14; Field No. 2662;
Matches 12; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
CY 1180 KPDPQMGCKKSKQLFSQVGVGVGSWSGWVVTHLELDGHKKKLRSPQI 1225
DB 871 KGGQGQQGQQQQPPQQSNLMGLGNTPDFALILIQGQQQQQQQQQAQV 916
RESULT 98
MRP6_RAT
ID MRP6_RAT STANDARD PRT: 1502 AA.
AC Q88269;
CD 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
FT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MULTIPLEG RESISTANCE-ASSOCIATED PROTEIN b (MRP-LIKE PROTEIN-1)
(MLP-1).
GN ABCG5 OR MRP6 OR MLPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; Tissue=liver;
MEDLINE=9279126; PubMed=9614210;
Hitachi T., Suzuki H., Ito Y., Ogawa K., Kume K., Shimizu T.,

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OX NCBI_TaxID 46617;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-91218158; PubMed-1708831;
 PT Tian G.L., Michel F., Macadre C., Slonimski P.P., Lazowska J.;
 PT "Principles of mitochondrial evolution in yeasts II. The complete
 PT sequence of the gene coding for cytochrome b in *Saccharomyces*
 RI douglasii reveals the presence of both new and conserved introns and
 RI discloses major differences in the fixation of mutations in
 RI evolution.";
 RI J. Mol. Biol. 218:747-763(1991).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS.
 CC -1- COFACTOR: TWO HEME GROUPS (H562 AND H566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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 CC
 CC EMBL: X59280; CAA11971.1;
 CC InterPro: IPR000179;
 CC Pfam: PF00032; Cytochrome_b_2; 1.
 CC ProSite: PS00193; Cytochrome_b_heme; 1.
 CC ProSite: PS00193; Cytochrome_b_heme; 1.
 CC Mitochondrion; Electron transport, Respiratory chain, Transmembrane;
 KW Heme.
 KW METAL 82 82 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 96 96 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 183 183 IRON 3 (HEME B562 AXIAL LIGAND).
 FT METAL 197 197 IRON 1 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 385 AA; 43631 MW; 3541b2d7d77e2602 CRC64;
 Query Match 0.5%; Score 59; DB 1; Length 385;
 Best Local Similarity 45.3%; Pct. Id. 22;
 Matches 14; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Q7 1929 PR061TFYELADPFAEKIKCITFLFACHLV 1459
 DB 271 PEWYLLDFYALRSIPKLLGVITMFAAILV 301
 RESULT 110
 CYB_YEAST
 ID CYB_YEAST STANDARD, FNT, 385 AA.
 AC 19563, Q95807, Q36301, Q55802,
 DT 21-JUL-1986 (Rel. 01, Created).
 DI 15-JUL-1998 (Rel. 36, Last sequence update)
 DF 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B,
 LN CYB OR CYTB
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*.
 OC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_TaxID 4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX STRAIN-D273-10B/A21;
 RC MEDLINE-81046788; PubMed-6254454;
 RA Reboredo F.G., Tzagoloff A.;
 PT "Assembly of the mitochondrial membrane system. DNA sequence and

RI organization of the cytochrome b gene in *Saccharomyces cerevisiae*
 RI D273-10B.";
 RI J. Biol. Chem. 255:9828-9837(1980).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=D273-10B/A21;
 PX MEDLINE-85660973; PubMed-6381594;
 RA Bonjardin C.A., Nobrega F.G.;
 RI "Revision of the nucleotide sequence at the last intron of the
 RI mitochondrial cytochrome b gene in *Saccharomyces cerevisiae*.";
 RI Praz J. J. Med Biol. Res. 17:17-20(1984).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=WR200;
 RX MEDLINE-95255283; PubMed-7737175;
 PA Claros M.G., Petrá J., Shu Y., Samatey F.A., Popot J.L., Jacq C.;
 RI "Limitations to in vivo import of hydrophobic proteins into yeast
 RI mitochondria. The case of a cytoplasmically synthesized apocytochrome
 RI b.";
 RI Eur. J. Biochem. 228:762-771(1995).
 RN [4]
 RN SEQUENCE OF 20-143 FROM N.A.
 RC STRAIN=777-3A;
 RX MEDLINE-81088336; PubMed-7001612;
 RA Lazowska J., Jacq C., Slonimski P.P.;
 PT "Sequence of introns and flanking exons in wild-type and box3 mutants
 PT of cytochrome b reveals an interlaced splicing protein coded by an
 PT intron.";
 RI Cell 22:333-348(1980).
 RN [5]
 RN SEQUENCE OF 144-169 FROM N.A.
 RC STRAIN=777-3A;
 PX MEDLINE-82115326; PubMed-7034963;
 RA Lazowska J., Jacq C., Slonimski P.P.;
 PT "Splice points of the third intron in the yeast mitochondrial
 PT cytochrome b gene.";
 RI Cell 27:12-14(1981).
 RN [6]
 RN MUTANT W7.
 RC MEDLINE-90005977; PubMed-2551731;
 PA Rivier-Chevillotte P., di Rago J.-P.;
 PT "Electron-transfer restoration by vitamin K3 in a complex
 PT III-deficient mutant of *S. cerevisiae* and sequence of the
 PT corresponding cytochrome b mutation.";
 RI FEBS Lett. 255:5-9(1989).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS.
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY
 CC
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 CC
 CC EMBL: J01476; AAA99924.1; ALT_SEQ.
 CC FMBL: X81042; CAA58863.1;
 CC FMBL: V00686; NOT_ANNOTATED_CDS.
 CC EMBL: J01473; AAA32151.2;
 CC EMBL: J01472; AAA32151.2; JOINED
 CC EMBL: J01475; AAA32152.2;
 CC EMBL: J01474; AAA32152.2; JOINED
 CC PIR: A00159; CBBY.
 CC SPT: S0007270; CBB.
 CC InterPro: IPR000179;

sclerosis patients.";
Am. J. Hum. Genet. 62:286-294(1998).
[12]
VARIANTS TSC.
RX Beauchamp R.L., Banwell A., McNamara P., Jacobsen M., Higgins E.,
Northrup H., Short M.P., Sims K., Ozellus L., Ramesh V.,
"Exon scanning of the entire TSC2 gene for germline mutations in 40
unrelated patients with tuberous sclerosis.",
Hum. Mutat. 12:408-416(1998).
[13]
VARIANTS TSC.
RX Gilbert J.R., Guy V., Kumar A., Wolpert C., Kandi R., Aylesworth A.,
Roses A.D., Pericak-Vance M.A.;
"Mutation and polymorphism analysis in the tuberous sclerosis 2 (TSC2)
gene.",
Neurogenetics 1:247-272(1999).
[14]
VARIANTS TSC, AND VARIANTS
RX Jones A.C., Shyamundar M.M., Thomas M.W., Maynard J.,
"Comprehensive mutation analysis of TSC1 and TSC2 and phenotypic
correlations in 150 families with tuberous sclerosis.",
Am. J. Hum. Genet. 64:1305-1315(1999).
[15]
VARIANT TSC ARG-717.
RX MEDLINE=90167238; PubMed=10069705;
Zhang H., Yamamoto T., Nanba E., Kikamura Y., Terada T., Akaboshi S.,
Yuasa I., Ohtani K., Nakamoto S., Takeshita K., Ohno K.;
"Novel TSC2 mutation in a patient with pulmonary tuberous sclerosis:
lack of loss of heterozygosity in a lung cyst.",
Am. J. Med. Genet. 82:368-370(1999).
[16]
VARIANTS TSC, AND VARIANTS
RX MEDLINE=20197627; PubMed=10735580;
Choy Y.S., Dabora S.L., Hall F., Ramesh V., Niida Y., Franz D.,
Kasprzyk-Obara J., Peave M.P., Fialkowski D.J.;
"Superiority of denaturing high performance liquid chromatography over
single-stranded conformation and conformation sensitive gel
electrophoresis for mutation detection in TSC2.",
Ann. Hum. Genet. 63:383-391(1999).
[17]
VARIANTS TSC, AND VARIANTS
RX MEDLINE=20067501; PubMed=10570913;
Chang H., Nanba E., Yamamoto T., Ninomiya H., Ohno K., Mizukuchi M.,
Takeshita K.;
"Mutational analysis of TSC1 and TSC2 genes in Japanese patients with
tuberous sclerosis complex.",
J. Hum. Genet. 44:391-396(1999)
[18]
VARIANTS TSC R-137; L-320; Q-611; N-647; P-717; E-769; M-963 w L-1657.
RX MEDLINE=20067501; PubMed=10570913;
Chang H., Nanba E., Yamamoto T., Ninomiya H., Ohno K., Mizukuchi M.,
Takeshita K.;
"Mutational analysis of TSC1 and TSC2 genes in Japanese patients with
tuberous sclerosis complex.",
J. Hum. Genet. 44:391-396(1999)
[19]
VARIANTS TSC W-e11.W-905; P-1744 w H 1745 R 1751 DEL, & VARIANT L 120.
RX MEDLINE=20076217; PubMed=10607950;
Yamashita Y., Ono J., Okada S., Wataya-Kaneda M., Yoshikawa K.,
Nishizawa M., Hirayama Y., Kobayashi E., Soyama K., Hino O.;
"Analysis of all exons of TSC1 and TSC2 genes for germline mutations
in Japanese patients with tuberous sclerosis: report of 10
mutations.",
Am. J. Med. Genet. 90:1245-1262(2000)
[20]
FUNCTIONS IMPLICATED AS A TUMOR SUPPRESSOR, MAY HAVE A FUNCTION IN
VESICULAR TRANSPORT, BUT MAY ALSO PLAY A ROLE IN THE REGULATION OF
CELL GROWTH APPET AND IN THE REGULATION OF TRANSCRIPTION MEDIATED
BY STEROID PEPTIDES. INTERACTION BETWEEN HAMARTIN AND TUBERIN MAY

FACILITATE VESICULAR DOCKING SPECIFICALLY STIMULATES THE
INTRINSIC GTPASE ACTIVITY OF THE RAS-RELATED PROTEIN RAP1A AND
RAB5, SUGGESTING A POSSIBLE MECHANISM FOR ITS ROLE IN REGULATING
CELLULAR GROWTH. MUTATIONS IN TUBERIN LEADS TO CONSTITUTIVE
ACTIVATION OF RAP1A IN TUMORS.
-1- SUBUNIT: INTERACTS WITH HAMARTIN. MAY ALSO INTERACT WITH THE
ADAPTOR MOLECULE RAP1A. THE FINAL COMPLEX CONTAINS TUBERIN
AND RAP1A. 5 LINKED TO RAB5 (PROBABLE).
-1- SUBCELLULAR LOCATION: CYTOPLASMIC. AT STEADY STATE FOUND IN
ASSOCIATION WITH MEMBRANES.
-1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS CAN BE DERIVED FROM
ALTERNATIVE SPLICING OF THE TSC2 GENE.
-1- TISSUE SPECIFICITY: LIVER, BRAIN, HEART, LYMPHOCYTES, FIBROBLASTS,
BILIARY EPITHELIUM, PANCREAS, SKELETAL MUSCLE, KIDNEY, LUNG AND
PLACENTA.
-1- DISEASE: DEFECTS IN TSC2 ARE THE CAUSE OF TUBEROUS SCLEROSIS
COMPLEX (TSC). THE MOLECULAR BASIS OF WHICH IS A FUNCTIONAL
IMPAIRMENT OF THE TUBERIN-HAMARTIN COMPLEX. TSC IS AN AUTOSOMAL
DOMINANT MULTI-SYSTEM DISORDER THAT AFFECTS ESPECIALLY THE BRAIN,
KIDNEYS, HEART, AND SKIN. TSC IS CHARACTERIZED BY HAMARTOMAS
(BENIGN OVERGROWTHS PREDOMINANTLY OF A CELL OR TISSUE TYPE THAT
OCCURS NORMALLY IN THE ORGAN) AND HAMARTIAS (DEVELOPMENTAL
ANOMALIES OF TISSUE DIFFERENTIATION). CLINICAL SYMPTOMS CAN RANGE
FROM BENIGN HYPOPIGMENTED MACULES OF THE SKIN TO PROFOUND MENTAL
RETARDATION WITH INTRACTABLE SEIZURES TO PREMATURE DEATH FROM A
Query Match 0.58; Score 59; DB 1; Length 1807;
Best Local Similarity 25.88; Pred. No. 5.3e+02;
Matches 17; Conservative 17; Mismatches 32; Indels 0; Gaps 0;
Q7 123 LMS:FTFMGAMVFLQVSTQVINFVTKMVPALIGSDGSEIEVSFNVEIVVKITSV 1382
Db 172 LSSEFLVLVNLVKNESCILDFYAPVQVQICILCVRTASSVDIEVSIQVLDVAVCYNCL 231
QY 1383 FVDALP 1388
Db 232 PAESLP 237
PESULT 129
FRAP_HUMAN STANDARD: PRT: 2549 AA.
AC P42345;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FRAP-PAPAMYCIN ASSOCIATED PROTEIN (FRAP) (PAPAMYCIN TARGET PROTEIN).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
PP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9427729; PubMed=8008069;
PA Brown E.J., Albers M.W., Shin T.B., Ichikawa K., Keith C.T.,
PA Lane W.S., Schreiber S.L.;
RT "A mammalian protein targeted by G1-arresting rapamycin-receptor
complex.",
EL Nature 369:756-758(1994)
FN [2]
RX X-RAY CRYSTALLOGRAPHY (2.7 Å RESOLUTION) OF 2018-2112
RX MEDLINE=96279639; PubMed=8662507;
PA Choi J., Chen J., Schreiber S.L., Clardy J.;
RT "Structure of the FKBP12-rapamycin complex interacting with the
binding domain of human FRAP.",
RL Science 273:239-242(1996).
[3]
RX X-RAY CRYSTALLOGRAPHY (2.7 Å RESOLUTION) OF 2018-2112.
RX MEDLINE=99190960; PubMed=10089303;
PA Liang J., Choi J., Clardy J.;
RT "Pellucid structure of the FKBP12-rapamycin-UKB ternary complex at 2.2

RA A resolution.

RT Act. Crystallized. D 55,746, 744(1999).

RL FUNCTION: ACTS AS THE TARGET FOR THE CELL-CYCLE ARREST AND IMMUNOSUPPRESSIVE EFFECTS OF THE FKBP12-RAPAMYCIN COMPLEX.

CC FUNCTION: BELONGS TO THE P13/P14-KINASES FAMILY.

CC SIMILARITY: CONTAINS 8 HEAT REPEATS.

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DR EMBL: L34075; AAA58486.1; .

DR PDB: 1FAP; 24-JUL-97.

DR PDB: INSG; 18 MAR 98.

DR PDB: 1AGE; 18 NOV 98.

DR MIM: 601241.

DR InterPro: IPR000403; .

DR Pfam: PF00454; P13_P14_kinase; 1.

DR PROSITE: PS00915; P13_4_KINASE_1; 1.

DR PROSITE: PS00916; P13_4_KINASE_2; 1.

DR PROSITE: PS00990; P13_4_KINASE_3; 1.

KW Transferase; Kinase; Repeat; 40-structure.

FT REPEAT 1; 16 53 HEAT 1.

FT REPEAT 2; 650 688 HEAT 2.

FT REPEAT 3; 659 897 HEAT 3.

FT REPEAT 4; 948 1025 HEAT 4.

FT REPEAT 5; 1069 1106 HEAT 5.

FT REPEAT 6; 1109 1148 HEAT 6.

FT REPEAT 7; 1150 1186 HEAT 7.

FT REPEAT 8; 1933 1970 HEAT 8.

FT DOMAIN 2188 2549 P13K/P14K.

SQ SEQUENCE 2549 AA: 258999 MW: 295616 KDa 9922AP4 QK264:

Query Match 0.5%, Score 59, DB 1, Length 2549.

Best Local Similarity 31.4%, Pred. No. 8,le-02.

Matches 11: Conservative 12, Mismatches 12, Indels 0, Gaps 0.

QY 2070 LKIPESSEVFPEAALIVIAIAERAKENIVLIP 2104

1111 1111 1111 1111 1111 1111

DE 1159 IWRILQSPETSTAMTSSIVFQKRYQIFIP 1193

RESULT 131

ID POLG_HCVI STANDARD: PRI: 3011 AA.

AC P26664;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE GLIEMO PROTEIN IN CHLAMYDIA TRACHOMATIS (G3E12). ENVELOPE GLYCOPROTEIN E2

DE ENVELOPE GLYCOPROTEIN E1 (G3E12) (G3E12). ENVELOPE GLYCOPROTEIN E2

DE (G668) (G668) (NSI). PROTEIN P7. NONSTRUCTURAL PROTEIN NS2 (P21)

DE 127 127 127 127 127 127

DE 127 127 127 127 127 127

DE NONSTRUCTURAL PROTEIN NS4A (P41). NONSTRUCTURAL PROTEIN NS4B (P27)

DE NONSTRUCTURAL PROTEIN NS5A (P56). NONSTRUCTURAL PROTEIN NS5B (P66)

DE (P70) (RNA-DIRECTED RNA POLYMERASE) (P70) (RNA-DIRECTED RNA POLYMERASE)

OS Hepatitis C virus (isolate 1) (HCV).

OC Viruses; ssRNA positive-strand viruses, no RNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_LoxID-11104;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE 91172626; PubMed 1848704;

RA Choo Q.-L., Richardson K.H., Han J.H., Berger K., Lee C., Imai C.,

RA Gallesco C., Coit D., Medina-Solby A., Barr P.J., Weiner A.J.,

RA Bradley D.W., Kuo G., Houghton M.

RT "Genetic organization and diversity of the hepatitis C virus."

RT Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).

RA Snyder S.H.

RT "RAT1: a mammalian protein that binds to FKBP12 in a rapamycin-dependent fashion and is homologous to yeast TOR1."

RL Cell 78:35-43(1994).

CC FUNCTION: ACTS AS THE TARGET FOR THE CELL-CYCLE ARREST AND IMMUNOSUPPRESSIVE EFFECTS OF THE FKBP12-RAPAMYCIN COMPLEX.

CC SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.

CC 1- SIMILARITY: CONTAINS 8 HEAT REPEATS.

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DR EMBL: L37085; AAA5929.1; .

DR EMBL: U11681; AAA20091.1; .

DR HSP: P42345; 1FAP.

DR InterPro: IPR000403; .

DR Pfam: PF00454; P13_P14_kinase; 1.

DR PROSITE: PS00915; P13_4_KINASE_1; 1.

DR PROSITE: PS00916; P13_4_KINASE_2; 1.

DR PROSITE: PS00990; P13_4_KINASE_3; 1.

KW Transferase; Kinase; Repeat.

FT REPEAT 1; 16 53 HEAT 1.

FT REPEAT 2; 650 688 HEAT 2.

FT REPEAT 3; 659 897 HEAT 3.

FT REPEAT 4; 948 1025 HEAT 4.

FT REPEAT 5; 1069 1106 HEAT 5.

FT REPEAT 6; 1109 1148 HEAT 6.

FT REPEAT 7; 1150 1186 HEAT 7.

FT REPEAT 8; 1933 1970 HEAT 8.

FT DOMAIN 2188 2549 P13K/P14K.

SQ SEQUENCE 2549 AA: 288791 MW: 288167 KDa 9986F99 QK664:

Query Match 0.5%, Score 59, DB 1, Length 2549.

Best Local Similarity 31.4%, Pred. No. 8,le-02.

Matches 11: Conservative 12, Mismatches 12, Indels 0, Gaps 0.

QY 2070 LKIPESSEVFPEAALIVIAIAERAKENIVLIP 2104

1111 1111 1111 1111 1111 1111

DE 1159 IWRILQSPETSTAMTSSIVFQKRYQIFIP 1193

RESULT 131

ID POLG_HCVI STANDARD: PRI: 3011 AA.

AC P26664;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE GLIEMO PROTEIN IN CHLAMYDIA TRACHOMATIS (G3E12). ENVELOPE GLYCOPROTEIN E2

DE ENVELOPE GLYCOPROTEIN E1 (G3E12) (G3E12). ENVELOPE GLYCOPROTEIN E2

DE (G668) (G668) (NSI). PROTEIN P7. NONSTRUCTURAL PROTEIN NS2 (P21)

DE 127 127 127 127 127 127

DE 127 127 127 127 127 127

DE NONSTRUCTURAL PROTEIN NS4A (P41). NONSTRUCTURAL PROTEIN NS4B (P27)

DE NONSTRUCTURAL PROTEIN NS5A (P56). NONSTRUCTURAL PROTEIN NS5B (P66)

DE (P70) (RNA-DIRECTED RNA POLYMERASE) (P70) (RNA-DIRECTED RNA POLYMERASE)

OS Hepatitis C virus (isolate 1) (HCV).

OC Viruses; ssRNA positive-strand viruses, no RNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_LoxID-11104;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE 91172626; PubMed 1848704;

RA Choo Q.-L., Richardson K.H., Han J.H., Berger K., Lee C., Imai C.,

RA Gallesco C., Coit D., Medina-Solby A., Barr P.J., Weiner A.J.,

RA Bradley D.W., Kuo G., Houghton M.

RT "Genetic organization and diversity of the hepatitis C virus."

RT Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).

CC -1- FUNCTION: THE SMALL PROTEIN NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- SUMMARY: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND RNA.
CC -1- SIMILARITY: THE PROTEIN BELONGS TO THE HELICASE FAMILY S29.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M62321; AAA45676.1; --
CC PIR: A39166; GNWVC3.
CC RSP: P27958; IHE1.
CC MEROPS: S29.001; --
CC MEROPS: S29.001; --
CC InterPro: IPR0000745; --
CC InterPro: IPR001490; --
CC InterPro: IPR002166; --
CC InterPro: IPR002519; --
CC InterPro: IPR002519; --
CC InterPro: IPR002521; --
CC InterPro: IPR002522; --
CC InterPro: IPR002531; --
CC InterPro: IPR002868; --
CC Pfam: PF01568; HCV_NS1; 1.
CC Pfam: PF01538; HCV_NS2; 1.
CC Pfam: PF01006; HCV_NS4a; 1.
CC Pfam: PF01303; HCV_NS4b; 1.
CC Pfam: PF01505; HCV_NS5a; 1.
CC Pfam: PF00998; HCV_RdRp; 1.
CC Pfam: PF01543; HCV_Capsid; 1.
CC Pfam: PF01542; HCV_core; 1.
CC Pfam: PF01539; HCV_env; 1.
CC Jolly: Jolly, G. et al. 1998. Transferrase, RNA-directed RNA polymerase;
CC Core protein; GAG protein; Envelope protein; Helicase; ATP-binding;
CC Transmembrane. Nonstructural protein NS2A. Sequence derived from the
CC INIT_MET 1 1
CC CHAIN 1 115
CC CHAIN 116 283
CC CHAIN 192 283
CC CHAIN 384 729
CC CHAIN 730 1006
CC CHAIN 1007 1615
CC CHAIN 1616 1962
CC CHAIN 1863 2913
CC CHAIN 2014 3011
CC CHAIN 347 369
CC CHAIN 1083 1083
CC ACT_SITE 1107 1107
CC ACT_SITE 1165 1165
CC NP_BIND 1230 1237
CC SITE 1316 1319
CC SITE 1316 1319
CC CARBOHYD 196 196
CC CARBOHYD 209 209
CC CARBOHYD 234 234
CC CARBOHYD 305 305
CC CARBOHYD 417 417
CC CARBOHYD 423 423
CC CARBOHYD 430 430
CC CARBOHYD 448 448
CC CARBOHYD 476 476
CC CARBOHYD 532 532
CC CARBOHYD 540 540
CC CARBOHYD 556 556
CC CARBOHYD 576 576

FT CARBOHYD 624 624 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 645 645 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 2041 2041 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 2077 2077 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 2249 2249 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 2364 2364 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 2789 2789 N-LINKED (GLCNAC) (POTENTIAL)
SQ SEQUENCE 3011 AA: 427117 MW: 455867bp5p577 CRC64;
Query Match 0.5%; Score 59; DB 1; Length 3011;
Best Local Similarity 34.5%; Pred. No. 9.8e+02;
Matches 10; Conservative q; Mismatches 10; Indels 0; Gaps 0;
QY 1821 VLLPAIKTKYKQIEKNWKNHMGPPMSILQ 1849
DB 1745 VIAPAVTNWOKLETFWAKHWNFISGIG 1773
RESULT 132
YHP9_YEAST STANDARD; PRT; 3744 AA.
AC P38811;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE HYPOTHEICAL 433.2 KDA PROTEIN IN HXT5-NPK1 INTERGENIC REGION.
GN YHR099W.
OS Saccharomyces cerevisiae (Baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycotina; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AR972;
PX MEDLINE-94378003; PubMed-8091229;
PA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
PA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
PA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
PA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
PA Nhan M., Pifkin L., Riles L., St. Peter H., Trevisan F., Vaughan K.,
PA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
PA Vaudin M.;
PA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
PA VIII.";
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: STRONG, TO S.POMBE SPAC1F5.11C.
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U00060; AAB68923.1; --
CC PIR: S46715; S46715.
CC SGD: S0001141; YHR099W.
CC KW Hypothetical protein; Transferase; Kinase.
CC DOMAIN 3414 3744 P13K/PI4K.
SQ SEQUENCE 3744 AA: 433171 MW: 4535867bp5p577 CRC64;
Query Match 0.5%; Score 59; DB 1; Length 3744;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1341 YSEGVINKTVKMWIPALIQNSQSIS 1366
DB 2907 HAFQVNNAYFLPALQOOSNSNI 2932

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DR EMBL: AE003512; AAF48985.1; ..
DR FlyBase: FBgn027358; Tim9.
KW Transport; Protein transport; Translocation; Mitochondrion;
KW Inner membrane.
SQ SEQUENCE 117 AA: 13520 MW: 3377A342075A57E5 CRC64:

Query Match 0.5%; Score 58; DB 1; Length 117;
Best Local Similarity 20.0%; Pred. No. 26;
Matches 12; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

QY 1143 CAGIVSSVSGTGVNAEEVRIETFPFAPFPIVIVVVFQKKMAGPKSGLFESVFWVS 1202
DB 42 CVDRCVTKTAPFNQNMKKVYVDVLTINAKPMEEENAKKAELQGPQEKRLKAAAI 101

RESULT 134
VNS1_BRSVA
ID VNS1_BRSVA STANDARD: PRT: 136 AA.
AC Q65694:
14 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NONSTRUCTURAL PROTEIN 1 (NONSTRUCTURAL PROTEIN 1C).
GN 1C OR NS1.
OS Bovine respiratory syncytial virus (strain A51908) (BRVS).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11247;
PP SEQUENCE FROM N.A.
RA MEDLINE=95146950; PubMed=7844532;
RA Pastey M.K., Samal S.K.;
PT "Nucleotide sequence analysis of the non-structural NS1 (1C) and NS2
PL (1B) protein genes of bovine respiratory syncytial virus."
CC J. Gen. Virol. 76:193-197(1995).
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CC or send an email to license@isb-sib.ch).
DR EMBL: U15947; AAA85671.1; ..
KW Nonstructural protein.
SQ SEQUENCE 136 AA: 15246 MW: AEB6A89D7BBD2B24 CRC64:

Query Match 0.5%; Score 58; DB 1; Length 136;
Best Local Similarity 28.1%; Pred. No. 31;
Matches 16; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

QY 161 FVLLPVKQCVPLAKETLTHCYKYLQCPMPFICSLVTKSVKVFAPYDSSALPLVLL 217
DB 77 FVSMPLIENSTYIWEIMELTHFQENQIHQNEELTFSSKPSSTIAKYSNGLSILL 144

RESULT 135
IL2_MUSSH
ID IL2_MUSSH STANDARD: PRT: 166 AA.
AC Q68867; P70462; P70463;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1995 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTEPLEKIN-2 PREPUSOR (II-2) (T-CELL GROWTH FACTOR) (TCGF).
GN IL2.
OS Mus musculus (Western white mouse).
OC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10096;
RN 111

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RESULT 136
TIM9_DROME
ID TIM9_DROME STANDARD: PRT: 117 AA.
AC Q9Y0V4:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9B.
GN TIM9B OR TIM9 OR C911747.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Epidrosocera; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 111

SEQUENCE FROM N.A.
RA Berger M.F., Branner M., Hartmann S.;
RA "Cloning and mapping of the Tim10/Tim9 gene family encoding small zinc
RA finger proteins involved in mitochondrial carrier import."
RA Submitted (MAY 1999) to the EMBL/Genbank/Trna databases
RN 121
SEQUENCE FROM N.A.
RA STRAIN BEKELEY:
RA MEDLINE=26196006; PubMed=10731142;
RA Adams M.L., Scholter S.F., Holt P.A., Evans C.A., Gecayene J.D.,
RA Amantides P.G., Schorer S.F., Li P.W., Hoskins P.A., Gallo P.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suttin G.G., Wortman J.K., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Roberts Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Ashayani A., An H.-J., Andrews-Pfannkuch C., Baldwin P.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Bergs P.V., Berman B.P., Bhandari C., Bolshakov S.,
RA Bolikova I., Botchan M.P., Boock J., Brackstein P., Brothier P.,
RA Burtis K.C., Busam B.A., Butler H., Castlen P., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke K., Davenport L.B., Davies P.,
RA DePallos B., DePiller A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Deason K., Deep L.E., Downes M., Duham-Rocha S., Dunkov R.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielson A.E., Gara N.S., Gelbart W.M., Glasser K.,
RA Gluspek A., Goad F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey E., Helms T.S., Hernandez T.P., Hengok J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kafush F., Karpen J.H., Ke Z., Kennison C.A., Ketchum K.A.,
RA Kimball R.K., Kishida C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lin X., Maltiel B., McIntosh T.C., Meleod M.P., McPherson D.,
RA Mekalanos J., Milshina N.V., Molnar C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy R., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskorn D.P., Pachob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Reinert K., Saunders R.B., Schaefer F., Shen H.,
RA Shue B.C., Stiden-Kimms L., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A., Stappleton M., Strong P., Sun F.,
RA Sztraskas R., Teeter C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z., Wassenaar D.A., Weinstock G.M., Weissent A.H.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhou X.H., Zhou F.N., Zhou X., Zhu S., Zhu X., Smith H.G.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RA Science 287:2185-2195(2000).
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DR EMBL: AF15104; AML43030.1; ..

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RP 107575; AAA34327.1;
RC EMBL: 041498; AAB39205.1; ALT_SEQ.
RC EMBL: 041495; AAB39207.1; ALT_SEQ.
RC MGI: 196548; 112.
DR InterPro: IPR000779; 1.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: R36245; INTERFERON2.
DR PROSITE: PS02424; INTERFERON2; 1
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 162 INTERFERON-2.
FT CARBOHYD 23 24 N-LINKED GLYCAN ) (BY SIMILARITY).
FT DISULFID 89 137 BY SIMILARITY.
FT DOMAIN 39 43 POLY-GLN.
FT VARIANT 24 27 MISSING.
FT SEQUENCE 166 AA; 18763 MW; C11056E29F386ARR CP064;

Query Match 0.5%; Score 58; DB 1; Length 166;
Best Local Similarity 20.2%; Pred. No. 40;
Matches 20; Conservative 25; Mismatches 56; Indels 6; Gaps 0;

QY 1718 LAEVTSTLEALAIPLQLSLPMSLLTMMKNTSELYSSEVYLLSALAALQKVVETLPHFTSP 1777
DB 6 LASCVTLLVLLVNSAIPSTSTSSSTSSIAACQOQHLEQLMDLGEILLSPENYNNL 65

QY 1778 YLEGLISGVIIHEKITSFMGSAQANIPITSEKTLATV 1816
DB 66 KLPMGLIKKFLVLPKATETKQGLLEDELGLPQGVLDLT 104

RESULT 136
RESP_GLOPE STANDARD; PRT; 189 AA.
AC P07445;
DT 01-AUG-1988 (rel. 08, Created)
DT 01-AUG-1988 (rel. 08, Last sequence update)
DT 01-MAY-1992 (rel. 22, Last annotation update)
DE RESOLVASE (ORF8).
GN RES.
OS Clostridium perfringens.

SEQUENCE OF 1-166 FROM N.A.
STRAIN SPRET/ET;
MEDLINE: 9430779; PubMed: 8319981;
Matesanz F., Alcina A., Pellicer A.;
"Existence of at least five interleukin-2 molecules in different
mouse strains.";
Immunogenetics 38:300-303(1993).
[2]
SEQUENCE OF 21-166 FROM N.A.
STRAIN=SPRET/ET;
MEDLINE: 96450482; PubMed: 8765095;
Matesanz F., Alcina A.;
"Glutamine and tetrapeptide repeat variations affect the biological
activity of different mouse interleukin-2 alleles.";
Eur. J. Immunol. 26:1675-1682(1996).
-1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
PROLIFERATION AND OTHER ACTIVITIES CRITICAL TO REGULATION OF THE
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL: 107575; AAA34327.1;
CC EMBL: 041498; AAB39205.1; ALT_SEQ.
CC EMBL: 041495; AAB39207.1; ALT_SEQ.
CC MGI: 196548; 112.
CC InterPro: IPR000779; 1.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: R36245; INTERFERON2.
CC PROSITE: PS02424; INTERFERON2; 1
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor.
CC FT SIGNAL 1 20 BY SIMILARITY.
CC FT CHAIN 21 162 INTERFERON-2.
CC FT CARBOHYD 23 24 N-LINKED GLYCAN ) (BY SIMILARITY).
CC FT DISULFID 89 137 BY SIMILARITY.
CC FT DOMAIN 39 43 POLY-GLN.
CC FT VARIANT 24 27 MISSING.
CC FT SEQUENCE 166 AA; 18763 MW; C11056E29F386ARR CP064;

Query Match 0.5%; Score 58; DB 1; Length 166;
Best Local Similarity 20.2%; Pred. No. 40;
Matches 20; Conservative 25; Mismatches 56; Indels 6; Gaps 0;

QY 1718 LAEVTSTLEALAIPLQLSLPMSLLTMMKNTSELYSSEVYLLSALAALQKVVETLPHFTSP 1777
DB 6 LASCVTLLVLLVNSAIPSTSTSSSTSSIAACQOQHLEQLMDLGEILLSPENYNNL 65

QY 1778 YLEGLISGVIIHEKITSFMGSAQANIPITSEKTLATV 1816
DB 66 KLPMGLIKKFLVLPKATETKQGLLEDELGLPQGVLDLT 104

RESULT 136
RESP_GLOPE STANDARD; PRT; 189 AA.
AC P07445;
DT 01-AUG-1988 (rel. 08, Created)
DT 01-AUG-1988 (rel. 08, Last sequence update)
DT 01-MAY-1992 (rel. 22, Last annotation update)
DE RESOLVASE (ORF8).
GN RES.
OS Clostridium perfringens.

Plasmid pIP404.
Bacteria, Firmicutes; Bacillus/Clostridium group, Clostridiaceae;
Clostridium.
NCBI_TaxID=1502;
[1]
SEQUENCE FROM N.A.
STRAIN=CPN50;
MEDLINE-88336297; PubMed-2901768;
Garnier T., Cole S.T.;
"Complete nucleotide sequence and genetic organization of the
bacteriocinogenic plasmid, pIP404, from Clostridium perfringens.";
Plasmid 19:134-150(1988).
[2]
SEQUENCE FROM N.A.
STRAIN=CPN50;
MEDLINE 88201476; PubMed-2996291;
Garnier T., Saurin W., Cole S.T.;
"Molecular characterization of the resolvase gene, res, carried by a
multicopy plasmid from Clostridium perfringens. Common evolutionary
origin for prokaryotic site-specific recombinases.";
Mol. Microbiol. 1:371-376(1987).
-1- FUNCTION: A LIKELY ROLE FOR THE RES PROTEIN WOULD BE TO STABILIZE
PIP404 BY REDUCING THE NUMBER OF PLASMID MULTIMERS RESULTING FROM
HOMOLOGOUS RECOMBINATION
CC -1- SIMILARITY: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC
RECOMBINASES.
CC
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CC
CC EMBL: Y00537; CAA68600.1;
CC EMBL: M32882; AAA98254.1;
CC PIR: S00869; S00869.
CC HSSP: P04012; 2RST.
CC InterPro: IPR001822;
CC Pfam: PF00239; recombinase; 1.
CC PROSITE: PS00397; RECOMBINASES_1; 1.
CC PROSITE: PS00398; RECOMBINASES_2; 1.
CC DNA recombination; DNA integration; DNA binding, plasmid.
CC ACT_SITE 9 9 TRANSIENT COVALENT LINKAGE TO DNA DURING
STRAND CLEAVAGE AND REJOINING
(BY SIMILARITY).
CC DNA_BIND 165 184 H-T-H MOTIF (PROBABLE).
CC SEQUENCE 189 AA; 21427 MW; B178138A1146D784 CP064;

Query Match 0.5%; Score 58; DB 1; Length 189;
Best Local Similarity 32.7%; Pred. No. 47;
Matches 16; Conservative 12; Mismatches 21; Indels 0; Gaps 0.

QY 1617 KRALDLNNKIQONISWKKTIIVTRFLKLPVDPDLAIVQRKKKEGEQAI 1665
DB 44 RQLDKMDELQEGDTVIITDLTRISRTKOLLNLDRIKAKGASIKSI 92

RESULT 137
VGLL_HSV6Z STANDARD; PRT; 250 AA.
AC P52526;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)
DE GLYCOPROTEIN L, PPEPNSOP
GN GL OR U82 OR CB10L.
OS Human herpesvirus (type 6 / strain 229) (HHV6).
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae,
Betaherpesvirinae; Roseolovirus.
CC NCBI_TaxID=36351;

```

```

FN SEQUENCE FROM N.A.
EX MEDLINE 90451233 PubMed 90451233
RA Juteau J, M., Levesque R.C.;
PA "Restriktion, endonuclease mapping and molecular cloning of the human
P1 herpesvirus, strain 229E49 genome."
RC Arch. Virol. 141:667-676 (1996).
EX FUNCTION ASSOCIATED WITH GLYCOPROTEIN B (GPB) TO FORM A COMPLEX
IMPACTANT FOR INFECTION AND CELL FUSION.
EX SIMILARITY TO OTHER HERPESVIRUSES GLYCOPROTEIN B.
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CC or send an email to license@sib-sib.ch).
```

EMBL: Z11899; CAA77952.1; -

HSSP: P20263; LOCP.

TRANSFAC: T91872; -

MIM: 164177; -

InterPro: IPR000327; -

InterPro: IPR001356; -

Plan: PF06346; Homeobox, 1.

Plan: PF00157; pou, 1.

PRINTS: PR00028; POU DOMAIN.

PROSITE: PS00027; HOMEBOX_1; 1.

PROSITE: PS00035; POU_1; 1.

ProSIP: PS00045; Pou_1; 1.

PROSITE: PS50071; HOMEBOX_2; 1.

Homeobox; DNA-binding; Transcription regulation; Nuclear protein;

Alternative splicing; Polymorphism.

DOMAIN 47 117 POU.

UNIQ 135 194 HOMEBOX.

VARIANT 227 227 T -> A.

VARIANT 262 262 M -> L.

FTID-VAR_003774.

FTID-VAR_003775.

SEQUENCE 265 AA; 36984 MW; 412211361RCEB2 CR064;

Query Match 0.5%; Score 58; DB 1; Length 265;

Best Local Similarity 44.0%; Pred. No. 70;

Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 622 AIVLSKSGICSLHLLRGWEEALEN 646

DB 94 ALQSPKMKCKRLPQLQKWEADN 118

RESULT 139

HLAL_HAEIN

ID HLAL_HAEIN STANDARD; PRT; 305 AA.

AC P33949;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUL-1994 (Rel. 38, Last annotation update)

DE BETA-LACTAMASE FOR-1 PRECURSOR (EC 3.5.2.6).

GN ROBI OR BIA.

OS Haemophilus influenzae, Pasteurella haemolytica, and

OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).

OG Plasmid R6b, and plasmid PAR2.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OC Haemophilus.

OX NCBI_TaxID=727, 75985, 715;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES-H influenzae; STRAIN=990; PLASMID=RR0b;

EX MEDLINE 90451233; PubMed 2201253;

RA Juteau J, M., Levesque R.C.;

RT "Sequence analysis and evolutionary perspectives of ROBI 1

RT beta-lactamase."

RL Antimicrob. Agents Chemother. 34:1354-1359 (1990).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES-P haemolytica; STRAIN=INPR 51; PLASMID=RR0b;

EX MEDLINE 91221591; PubMed 2024356;

RA Livrelli V., Peduzzi J., Joly B.;

RT "Sequence and molecular characterization of the ROBI 1 beta-lactamase

RT gene from Pasteurella haemolytica."

RL Antimicrob. Agents Chemother. 35:242-251 (1991).

RN [3]

RP SEQUENCE FROM N.A.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 TISSUE: Kidney;
 MEDLINE 93027169; PubMed 1138763;
 RA Takada J., Saito S., Bell G.I.;
 RT "Human OCT3 gene family: cDNA sequences, alternative splicing, gene
 RI organization, chromosomal location, and expression at low levels in
 RI adult tissues.";
 RI Nucleic Acids Res. 20:4613-4620(1992).
 RN [2]
 RP SEQUENCE OF 188-274 FROM N.A.
 RP TISSUE: Heart, and Skeletal muscle;
 RP MEDLINE 94192665; PubMed 7938264;
 RA Wey E., Lyons G.E., Schaefer E.W.;
 RT "A human p60 domain gene, mbp60, is expressed in developing brain and
 RI specific adult tissues.";
 RI Eur. J. Biochem. 220:753-762(1994).
 RN [3]
 RP SEQUENCE OF 212-283 FROM N.A.
 RP MEDLINE 96160536; PubMed 8567814;
 RA Abdel-Rahman B., Fiddler M., Rappolee D., Pergament E.;
 RT "Expression of transcription regulating genes in human
 RI preimplantation embryos.";
 RI Hum. Reprod. 10:2787-2792(1995).
 RN [4]
 RP FUNCTION, TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF
 CC ("ATTTCGAT"). PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL
 CC GENE.
 CC
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; OCT-3A (SHOWN HERE) AND OCT-3B
 CC (AC P31359); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC
 CC -1- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS BELONGS
 CC TO CLASS-5 POU.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z1198; CAA77951.1;
 CC EMBL: Z4193; CAA77974.1;
 CC EMBL: Z21964; CAA79975.1;
 CC EMBL: S81255; AAB35990.1;
 CC FTR: S25561; S25561.
 CC USSP: P20263; 102P.
 CC TRANSFAC: T00652;
 CC MIM: 164177;
 CC InterPro: IPR000327;
 CC InterPro: IPR001356;
 CC Pfam: PF00046; homeobox, 1.
 CC PRINTS: PF00157; pou, 1.
 CC PROSITE: PS00028; P40DOMAIN.
 CC PROSITE: PS00027; HOMEBOX_1, 1.
 CC PROSITE: PS00035; POU_1, 1.
 CC PROSITE: PS00465; POU_2, 1.
 CC PROSITE: PS00071; HOMEBOX_2, 1.
 CC Homeobox: DNA-binding; Transcription regulation, Nuclear protein;
 CC Alternative splicing.
 CC
 CC FT DOMAIN 142 212 POU.
 CC FT DNASBIND 230 289
 CC FT COREFLCT 189 289 A -> G (IN REF. 2; Z21963).
 CC FT CONFLICT 220 220 I -> T (IN REF. 2; Z21963).
 CC FT CONFLICT 227 227 V -> L (IN REF. 2; Z21963).
 CC FT CONFLICT 230 230 R -> C (IN REF. 2; Z21964).
 CC FT CONFLICT 240 240 R -> Q (IN REF. 2; Z21964).
 CC FT CONFLICT 251 251 Q -> R (IN REF. 2; Z21964).
 CC FT CONFLICT 276 276 V -> W (IN REF. 3).
 CC SEQUENCE 360 AA; 38570 MW; 934558DAEAC0535B CRC64;

Query Match 0.5%; Score 58; DB 1; Length 360;
 Best Local Similarity 44.0%; Pred. No. 1e+02;
 Matches 15; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 622 ATVTSKSGTSHPTIPGWEEALEN 646
 DE 189 ALGSPKNCCKLPPILOKWEVADN 213
 ID SYDI_RAT
 AC 055145;
 DT 15-JUL-1999 (Rel. 38, Created)
 RESULT 145
 SYDI_RAT
 ID SYDI_RAT
 AC 055145;
 DT 15-JUL-1999 (Rel. 38, Created)
 NPL4_HUMAN
 ID NPL4_HUMAN
 STANDARD: PRT; 375 AA.
 AC Q9733;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2)
 DE (NAP2).
 GN NAPI14 OR NAP2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE 97081759; PubMed 8939009;
 RA Hu R.-J., Lee M.P., Johnson L.A., Feinberg A.P.;
 RT "A novel human homologue of yeast nucleosome assembly protein, 65 kb
 RI centromeric to the p57KIP2 gene, is biologically expressed in fetal
 RI and adult tissues.";
 RI Hum Mol Genet 5:1743-1748(1996).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC
 CC -1- TISSUE SPECIFICITY: UTRICULAR, BILATERALLY EXPRESSED IN FETAL
 CC AND ADULT TISSUES. HIGHEST LEVELS IN TESTIS.
 CC
 CC -1- SIMILARITY: BELONGS TO THE NUCLEOSOME ASSEMBLY PROTEIN (NAP)
 CC FAMILY.
 CC
 CC -1- SIMILARITY: TO HUMAN SET PROTEIN
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: 977456; AAC00870.1;
 CC FTR: 601651;
 CC IPIREF: IPI002164;
 CC Pfam: PF00956; NAP_family; 1.
 CC
 CC KW Nuclear protein.
 CC FT DOMAIN 126 131 POLY-GLU.
 CC FT DNASBIND 265 271 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
 CC FT DOMAIN 301 310 ASP/GLU-RICH (ACIDIC).
 CC FT DOMAIN 347 370 ASP/GLU-RICH (ACIDIC).
 CC SEQUENCE 375 AA; 42823 MW; 788E1F9F5E8F045 CRC64;

Query Match 0.5%; Score 58; DB 1; Length 375;
 Best Local Similarity 31.2%; Pred. No. 1e+02;
 Matches 15; Conservative 8; Mismatches 25; Indels 0; Gaps 0;
 QY 1743 TPTMPSITITMKNTSHIVSSEVVIISALAKVKVETLPHFISPYLE 1780
 DE 16 VPSISVFAAKNASNTFKITTCVMGNPRVLAALQERLDNVHTPSSYLE 57
 ID SYDI_RAT
 AC 055145;
 DT 15-JUL-1999 (Rel. 38, Created)


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QY 1519 SFMSQLSSNNLKKVWESGPHHLEKLEKLELLETVL 1555
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38 SGRSRLFTNFGRLTSSGNSNYGYTRKSTSL 74
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 147
YXK7_CAEEL STANDARD; PRT; 397 AA.
ID YXK7_CAEEL
AC G18674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 40-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL 45.9 KDA PROTEIN C47E12.7 IN CHROMOSOME IV.
GN C47E12.7;
OS
OC Eukaryota; Metazoa; Nemata; Chromadorea; Phaditilia; Phaditoidae;
OC Rhaditidae; Pelodierinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BR1575G.H2;
RA Coles L.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RV REVISIONS
RP STRAIN BRISTOL N2;
RC Burstin R.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases
OC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE NNP-1 FAMILY.
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-----
EMBL: Z68882; CAA93111.1; -.
DB Wormpep; C47E12.7; CE29571;
KW Hypothetical protein, Nuclear protein.
SQ SEQUENCE 397 AA; 45870 MW; 03E91E2D26D7D6BC CRC64;

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Query Match 0.58; Score 58; DB 1; Length 397;
Best Local Similarity 21.58; Prod. No. 1.3e+02;
Matches 14; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

QY 560 IFQAEISKNGEWEVLEKIAADHIIKEEILSENQVQVLLPFVWVNNQTFESNM 619
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 146 VFQETTTSTDKSFNFKLFRFPASIIIDELDAAGGLTKKQVIACLKPYTELGNKDISEYL 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 520 KIAIY 624
   ||
DB 206 FISLY 210
   ||

RESULT 148
KCCL_EMENI STANDARD; PRT; 414 AA.
ID KCCL_EMENI
AC Q00771;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CALCULUM/CAAL-06611H DEFICIENT PROTEIN KINASE (EC 2.7.1.123) (CMFE).
GN CMKA.
OS
OC Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Emericetia; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OC NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.

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RX MFQULNF-92235350; PubMed-1563634;
RA Kornstein L.B., Gaiso M.L., Hammell R.J., Bartlett D.C.;
RT Cloning and sequence determination of a cDNA encoding Aspergillus
RT nidulans calmodulin-dependent multifunctional protein kinase.;
RL Gene 113-75-82(1992)
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
-----
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-----
EMBL: M74120; AAB97502.1; -.
DB HSSP; Q63450; 1A06.
DR InterPro; IPR000719; -.
DR InterPro; IPR0002290; -.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00138; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW phosphorylation; ATP-binding
FT DOMAIN 23 278 PROTEIN KINASE.
FT NIP-BIND 29 37 ATP (BY SIMILARITY).
FT BINDING 50 50 ATP (BY SIMILARITY).
FT ACT_SITE 142 142 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT SEQUENCE 411 AA; 45889 MW; 1F8D58A1C0B2F18C CRC64;

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Query Match 0.58; Score 58; DB 1; Length 414;
Best Local Similarity 48.38; Prod. No. 1.3e+02;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1471 LKLPKRFETTPKAVSFNKSQEE 1495
   ||| ||| ||| ||| ||| ||| ||| |||
DB 317 LKMQEEDDEEDIPSADVQVQVASFASW 341
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 149
AATL_ARATH STANDARD; PRT; 430 AA.
ID AATL_ARATH
AC P46643;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PEPHYRSOR (EC 2.6.1.1)
DE (TRANSAMINASE A).
GN ASPL OR AT2G30970 OR F7F1.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliopsida; Eudicotyledons; Core eudicotids; Rosidae; eurosids II;
OC Brassicaceae; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE=Leaf;
RX REDLINE 95201829; PubMed 7894512;
RA Schuster C.J., Ceruzzi G.M.;
RT "The aspartate aminotransferase gene family of Arabidopsis encodes
RT isoenzymes localized to three distinct subcellular compartments.";
RL plant J. 7:61-75(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE-20083487; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Renito M.-L., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Baustead M.E., Feldblum T.V.,

```


SEQUENCE FROM N.A.
MEDLINE: 92050809; PubMed: 1834974;
Jansson J.W.G., Schulz A.S., Steenvoorden A.C.M., Schmidberger M.,
Strochi S., Ambros P., Bartram C.R.;
"A novel putative tyrosine kinase receptor with oncogenic potential.";
Oncogene 6:2113-2120(1991).
[2]
SEQUENCE FROM N.A.
MEDLINE: 92017777; PubMed: 1656226;
Bryan J.P., Frye R.A., Codswell P.C., Neubauer A., Kitch B.,
Prokop C., Espinosa R., le Beau M.M., Earp H., Liu E.T.;
"AXL, a transforming gene isolated from primary human myeloid
leukemia cells, encodes a novel receptor tyrosine kinase.";
Mol. Cell. Biol. 11:5016-5031(1991).
[4]
SEQUENCE OF 667-723 FROM N.A.
MEDLINE: 94067791; PubMed: 9247543;
Lee S.-I., Strunk K.M., Spritz K.A.;
"A survey of protein tyrosine kinase mRNAs expressed in normal human
melanocytes.";
Oncogene 8:1403-1410(1993).
-1- FUNCTION. MAY FUNCTION AS A SIGNAL TRANSDUCER BETWEEN SPECIFIC
CELL TYPES OF MESODERMAL ORIGIN.
-2- CATALYTIC ACTIVITY: ATP, A PROTEIN TYROSINE - ADP, PROTEIN
TYROSINE PHOSPHATE.
-3- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-4- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-5- DISEASE. HAS TRANSFORMING POTENTIAL IN PATIENTS WITH CHRONIC
MYELOPROLIFERATIVE DISORDER OR CHRONIC MYELOIDIC LEUKEMIA.
-6- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
-7- SIMILARITY: CONTAINS 2 IMMUGLOBULIN LIKE C2 TYPE DOMAINS.
-8- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III LIKE DOMAINS.
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or send an email to license@sib.sib.ch).
EMBL: X57019; CAA60338.1; ALT_INIT.
EMBL: M76125; AAB61243.1; ALT_INIT.
EMBL: S65125; AAB20305.1; ALT_INIT.
HSSP: P11362; IFGL.
MIM: 109135;
InterPro: IPR000719;
InterPro: IPR001245;
InterPro: IPR001777;
InterPro: IPR003006;
Pfam: PF00041; I03; 2;
Pfam: PF00047; I03; 2;
Pfam: PF00069; pkinase; 1;
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1;
PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
Receptor: Glycoprotein; Tyrosine-protein kinase, ATP binding;
transferase; phosphorylation, Transmembrane, Signal; Repeat;
Immunoglobulin domain; proto-oncogene; Alternative splicing.
FT CHAIN 1 18
FT CHAIN 19 887
FT DOMAIN 19 444
FT TRANSMEM 445 465
FT DOMAIN 466 887
FT DOMAIN 42 117
FT DOMAIN 146 205
FT DOMAIN 217 315
FT DOMAIN 319 416
FT DOMAIN 529 890
FT DOMAIN 535 543
FT NP_BIND 548 548
FT BINDING 560 560
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).

ACT_SITE 665
DISULFID 49 110
DISULFID 153 198
CARBOHYD 36 36
CARBOHYD 150 150
CARBOHYD 191 191
CARBOHYD 332 332
CARBOHYD 338 338
CARBOHYD 394 394
MOD_RES 696
VARSPIC 422 430
CONFLICT 296
CONFLICT 331 331
CONFLICT 632 632
SEQUENCE 887 AA; 97374 MW; 24/RECI646298EDA Cko04;
Query Match 0.58; Score 58; DR 1; Length 887;
Best Local Similarity 25.00; Pos: 30;2;
Matches 15; Conservative 15; Mismatches 30; Indels 0; Gaps 0;
CY 1210 CEEGQHKKELESQILVPT; EML SEC; FVLPQFQFQFHEVYFQV IISQINIQV; SPS 1269
DB 751 IYVYLPQCNKQKQAPDGLGIALMSRWELNPDQRFSTFELREDLENTLKALPPAQEPD 810
RESULT 164
IP2_CHAIN STANVAPD PPT: 892 AA.
AC 084098;
DT 30-MAY-2000 (Rel 39, Created)
DT 30-MAY-2000 (Rel 39, Last sequence update)
DT 30-MAY-2000 (Rel 39, Last annotation update)
DE TRANSLATION INITIATION FACTOR IF-2.
GN INEB OR CT096.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
PP SEQUENCE FROM N.A.
PC STEFAN F.V.W. 3/95;
PX MEDLINE: 94000809; PubMed: 9784136;
PA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe P., Aravind L.,
Mircheff W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
Science 282:754-759(1998).
RL -1- FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION
OF PROTEIN SYNTHESIS IN VITRO, PROMOTES FORMYL-METHIONYL-TRNA FROM
CC SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S
CC RIBOSOMAL SUBUNIT. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP
CC DURING THE FORMATION OF THE 70S RIBOSOMAL COMPLEX (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
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CC entities requires a license agreement (see <http://www.isb-sib.ch/4000000>
CC or send an email to license@sib.sib.ch).
CC EMBL: AE001283; AAC67687.1;
CC InterPro: IPR000178;
CC InterPro: IPR000795;
CC Pfam: PF00009; GTP_EFTD; 1.
CC Pfam: PF02131; IF2; 1.
CC PROSITE: PS01176; IF2; 1.
CC Initiation factor; Protein biosynthesis; GTP-binding.
FT DOMAIN 400 548
FT NP_BIND 406 413
FT BINDING 413 413
GTP (BY SIMILARITY).

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EMBL: Z46791; CAAB6762.1; -.
EMBL: Z46792; CAAB6763.1; JOINED.
EMBL: Z46793; CAAB6764.1; -.
EMBL: Z46794; CAAB6765.1; JOINED.
EMBL: Z46795; CAAB6766.1; JOINED.
EMBL: Z46796; CAAB6767.1; JOINED.
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EMBL: Z46798; CAAB6769.1; JOINED.
EMBL: Z46799; CAAB6770.1; JOINED.
EMBL: Z46800; CAAB6771.1; JOINED.
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EMBL: Z46848; CAAB6819.1; JOINED.
EMBL: Z46849; CAAB6820.1; JOINED.
EMBL: Z46850; CAAB6821.1; JOINED.
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EMBL: Z46955; CAAB6926.1; JOINED.
EMBL: Z46956; CAAB6927.1; JOINED.
EMBL: Z46957; CAAB6928.1; JOINED.
EMBL: Z46958; CA

RC TISSUE brain;
KA Lopez-Pedraza C., Azamburu E., Pakeman A.S., Copeland N.G.,
Gilbert D.J., Thomas S., Distelhorst C., Jenkins N.A., Rao A.,
RT "REAS: The RE-AT family of transcription factors expands in a new
KL direction.";
KL Cold Spring Harb. Symp. Quant. Biol. 64:517-526(1999).
RN [5].
RN SEQUENCE OF 675 1531 FROM N.A.
RC TISSUE-brain; PDB-id 1Q565528;
EX MEDLINE 2002/2/29; PubMed 10765528;
KA Eschke C., Kuhl E., Jahnsmeyer A., Grosschik E.H., Schweitzer E.;
RT "Isolation and characterization of novel CAG repeat containing genes
KL expressed in human brain.";
KL DNA Seq. 10:1-6(1999).
CC -1- FUNCTION: PLAYS A ROLE IN THE REGULABLE EXPRESSION OF GENES.
CC REGULATES HYPERONICITY-INDUCED CELLULAR ACCUMULATION OF
CC OSMOLYTES.
CC -1- SUBUNIT: DOES NOT BIND WITH PDS AND JUN TRANSCRIPTION FACTORS. BUT
CC MIGHT BE CAPABLE OF FORMING STABLE DIMERS WITH DNA ELEMENTS.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE SPLICING: 3 ISOTYPES: A, B AND C (SHOWN HERE): MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE, BRAIN,
CC HEART AND PERIPHERAL BLOOD LEUCOCYTES. ALSO EXPRESSED IN PLACENTA,
CC LUNG, LIVER, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS,
CC OVARY, SMALL INTESTINE AND COLON.
CC -1- SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
CC -1- CAUTION: REF.5 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1165
CC ONWARD DUE TO A FRAMESHIFT.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AB020634; BAA74850.1; -;
CC EMBL: AF089824; AAD18136.1; -;
CC EMBL: AF134870; AAD38360.1; -;
CC EMBL: Z97016; CAB09693.1; ALT_FRAME.
CC EMBL: AF163836; AAD48441.1; -;
CC MIM: 604708; -;
CC INTERPRO: IPR000451; -;
CC PROSITE: PS01284; REL.1; PALM_NRG.
CC PROSITE: PS0254; REL.2; 1.
CC Transcription regulation; Activator; Nuclear protein; DNA-binding;
KW Alternative splicing.
KW DOMAIN 69 100 SER-RICH.
FT DOMAIN 293 350 DNA BINDING.
FT DOMAIN 739 743 POLY GLR.
FT DOMAIN 879 888 POLY-GLN.
FT DOMAIN 966 971 POLY-THR.
FT DOMAIN 1248 1266 POLY-GLN.
FT VARSPLIC 1 76 MISSING (IN ISOFORM A).
FT VARSPLIC 1 47 MISSING (IN ISOFORM B).
FT C-REPEAT 1369 1369 E > D (IN REF. 5).
SQ SEQUENCE 1531 AA; 165764 MW; A686508080A8B69E CR664;

Query Match 0.58; Score 58; DB 1; Length 1531;
Best Local Similarity 26.49; Pred. No. 60+02;
Matches 19; Conservative 14; Mismatches 36; Indels 6; Gaps 0;
QY 123 CHLDRGSLGALVITHTETLIVPVVQLKFKRKEPWEHLFVPSQVPLAKPTLTHC 192
DB 496 MELPHONHLLVAVTPYDHQHTLTPSVGVIVVTNAGSHUDGPFYTYTTPDAAGALNVNV 555
QY 184 VKDLGFMDFGCS 194
DB 556 KREISSVAKPCS 567

RESULT 175
POLG_POL2W
TD POLG_POL2W STANFAPC PPT: 2205 AA.
AC P23069;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Pol 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPEPTIDE [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS
DE P2A TO P2C, P3A: GENOME-LINKED PROTEIN VP6; PICORNAIN 3C
DE (PC 3, 4, 22, 28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P40
DE (PC 2, 7, 7, 48)]
OS Poliovirus type 2 (strain W-2).
OC Viruses; ssRNA positive strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus
OX NCBI_TaxID:12085;
RN [1]
FP SEQUENCE FROM N.A
FX MEDLINE 90155230; PubMed 2154539;
FA Pevsner J.C., Oh C.K., Cunningham E.L., Calenoff M., Jubelt R.;
RT "Localization of genomic regions specific for the attenuated, mouse-
PL adapted poliovirus type 2 strain W-2.";
PL J. Gen. Virol. 71:41-52(1990).
CC -1- FUNCTION: 73C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC Q/Q SITES IN THE POLYPEPTIDE. IT MAY BE A CYSTEINE PROTEASE.
CC -1- SUBUNIT: THE VPUS/CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS.
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: D00625; BAA00516.1; ALT_SEQ.
CC FTR: A34832; GNRV2W.
CC HSP: P04299; IPOV.
CC MSKOPS: C03.001; -;
CC MSKOPS: C03.020; -;
CC INTERPRO: IPR000081; -;
CC INTERPRO: IPR000149; -;
CC INTERPRO: IPR000605; -;
CC INTERPRO: IPR001205; -;
CC INTERPRO: IPR001676; -;
CC INTERPRO: IPR002527; -;
CC Pfam: PF00548; Cys protease-3C; 1.
CC Pfam: PF00947; Pico_P2A; 1.
CC Pfam: PF01552; Pico_P2B; 1.
CC Pfam: PF00680; RNA_dep_RNA_pol; 1.
CC Pfam: PF00910; RNA_helicase; 1.
CC Pfam: PF00073; rhv; 3.
CC Polyprotein; Core protein; Transferase;
KW RNA-directed RNA polymerase, P3C-class, E3C1, protease, Myristate.
FT CHAIN 2 69
FT CHAIN 70 340 COAT PROTEIN VP4 (PIA).
FT CHAIN 341 578 COAT PROTEIN VP2 (PIB).
FT CHAIN 579 879 COAT PROTEIN VP1 (PID).
FT CHAIN 880 1028 PROTEASE 2A.
FT CHAIN 1029 1125 CORE PROTEIN 2B.
FT CHAIN 1126 1454 CORE PROTEIN 2C.
FT CHAIN 1455 1541 CORE PROTEIN 3A.
FT CHAIN 1542 1563 GENOME-LINKED PROTEIN VP6.
FT CHAIN 1564 1746 PICORNAIN 3C.
FT CHAIN 1747 2205 RNA-DIRECTED RNA POLYMERASE 3D.
FT LIPID 2 2 MYRISTATE (HY SIMILARITY).
FT ACT_SITE 1710 1710 PROTEASE (POTENTIAL).
FT ACT_SITE 1724 1724 PROTEASE (POTENTIAL).
SQ SEQUENCE 2205 AA; 245701 MW; 2A42AR039F0254AD CR664;

Query Map 4: (KW) Score 58; ID 1; Length 2207;
 Best Local Similarity: 22.29; Pred. No. 9, 2e-02;
 Map 405: 18; Conservative 15; Mismatches 46; Indels 0; Gaps 0

QY 481 TSLMISLHRTAFVRLAMRHKKINKSKKGVTSFKEAVLAKGCHLHVLSALGA 540
 DE 623 JAVELGAINVPSIVLPHVITGQIPSEFVSFFADGAVATVVDATKRSKL 682
 QY 541 FEFKRFESSEVTISNLNLF 561
 DE 683 FSVWKLIVKDTVQLRRKLEFF 703

Query Match: 0.58; Score 58; ID 1; Length 2207;
 Best Local Similarity: 22.29; Pred. No. 9, 2e-02;
 Matches 18; Conservative 15; Mismatches 46; Indels 0; Gaps 0

QY 481 TSLMISLHRTAFVRLAMRHKKINKSKKGVTSFKEAVLAKGCHLHVLSALGA 540
 DE 623 JAVELGAINVPSIVLPHVITGQIPSEFVSFFADGAVATVVDATKRSKL 682
 QY 541 FEFKRFESSEVTISNLNLF 561
 DE 683 FSVWKLIVKDTVQLRRKLEFF 703

RESULT 177
 MYSJ_DICD1
 ID MYSJ_DICD1 STANDARD; PRT: 2245 AA.
 AC P54697;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MYOSIN II HEAVY CHAIN.
 GN MYO3.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID 44689;
 RN [1]
 RC SEQUENCE FROM N.A.
 RE STRAIN AX4;
 RA MEDLINE-96215148; PubMed-8636147;
 RA Hammett J.A., Liu, J., Jung G.;
 RT "The sequence of the dictyostelium myo-J heavy chain gene predicts a novel, dimeric, unconventional myosin with a heavy chain molecular mass of 258 kDa."
 FT J. Biol. Chem. 271:7120-7127(1996).
 RL [2]
 RP SEQUENCE OF 1-1021 FROM N.A.
 RX MEDLINE-97039016; PubMed 8884397;
 RA Peterson M.D., Griest A.S., Titus M.A.;
 RT "Dictyostelium discoideum myof: a member of a broadly defined myosin V class of a class XI unconventional myosins";
 RL J. Muscle Res. Cell Motil. 17:411-424(1996).
 RN [3]
 RP SEQUENCE OF 182-298 FROM N.A.
 RX MEDLINE 9502929; PubMed 7957787;
 RA Titus M.A., Kuspa A., Loomis C.F.;
 RT "Discovery of myosin genes by physical mapping in Dictyostelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9440-9450(1994).
 CC -1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CLASS 5 MYOSINS.
 CC -1- SIMILARITY: CONTAINS 3 TO DOMAINS.
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01 01-NOV-2000 (Rel. 40, Last sequence update)
 02 01-NOV-2000 (Rel. 40, Last annotation update)
 03 PROTEASOME SUBUNIT BETA TYPE 1 (P01343-46) (2003 PROTEASOME ALPHA
 04 SUBUNIT F) (PROTEASOME COMPONENT C5) (FAS-F22/FAFP98).
 05 P01343-46 (14-21-2000).
 06 Arabidopsis thaliana (Mouse-ear cress).
 07 Eukaryote: Viridiplantae: Eremyophyta: Fractophyta: Spermatophyta;
 08 Mammaliophyta: euarchontyleons: core eudicots: Rosidae: eurosids 11;
 09 Brassicales: Brassicaceae: Arabidopsis.
 10 NBI_LUXID 4702;
 11 [1]
 12 SEQUENCE FROM N.A.
 13 STRAIN: CV_040081A; L1550F; Length: 259 AA.
 14 MEDLINE: 96078945; PubMed: 79874125.
 15 Guschik F., Janet F., Phillips G., Farnetier Y., Ghoul C.,
 16 Fieck J.
 17 "Molecular characterization of a beta-type proteasome subunit from
 18 Arabidopsis thaliana co-expressed at a high level with an alpha-type
 19 proteasome subunit early in the cell cycle."
 20 Plant J. 6:537-546(1994).
 21 [2]
 22 SEQUENCE FROM N.A.
 23 STRAIN: CV_040081A;
 24 MEDLINE: 96278790; PubMed: 9611184;
 25 Fu H., Boelling J.H., Arnold C.S., Hochstrasser M., Viorstra R.D.
 26 "Molecular organization of the 20S proteasome gene family from
 27 Arabidopsis thaliana."
 28 Genetics 149:677-692(1998).
 29 [4]
 30 SEQUENCE FROM N.A.
 31 STRAIN: CV_040081A;
 32 Christen N., Robert P., Brattier P., Winkler P., Cattalini L.,
 33 Attardou P., Saurin W., Weissmann T., Meuwis H.W., Redl S.,
 34 Demme P., Mayer P., Viorstra R., Viorstra R., Viorstra R.,
 35 Submitted (May 2000) to the EMBL/GenBank/TrEMBL databases.
 36 FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 37 WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,
 38 PHE, LEU, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR
 39 SLIGHTLY BASIC pH. THE PROTEASOME HAS AN ATP-DEPENDENT PEPTIDYL-
 40 ACTIVITY.
 41 PATHWAY: INVOLVED IN AN ATP-DEPENDENT DEPENDENT NON-LYSOSOMAL
 42 PROTEOLYTIC PATHWAY.
 43 SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON-IDENTICAL
 44 SUBUNITS WHICH FORM A HEPTAMERIC CORE SURROUNDED BY REGULATORY
 45 SUBUNITAR LOCALIZED CYTOSOLIC AND NUCLEAR (BY SIMILARITY).
 46 TISSUE SPECIFICITY: PRESENT IN ALL TISSUES EXAMINED. SLIGHTLY
 47 LOWER LEVELS IN FETUS.
 48 DEVELOPMENTAL STAGE: EXPRESSED AT MAXIMAL LEVELS AFTER FIRST DAY
 49 OF CELL GROWTH.
 50 SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11B; ALSO KNOWN AS THE
 51 PROTEASOME B-TYPE FAMILY.

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 contact the EMBL/GenBank/TrEMBL databases or send an email to license@ebi.ac.uk.

EMBL: X67446; CAA47753.1; AL1_1011;
 EMBL: X79909; CAA5201.1; AL1_1011;
 EMBL: AF04547; AA02073.1;
 EMBL: AF04547; CAA02066.1;
 EMBL: F011066;
 InfoProc: IP0000243;
 InfoProc: IP0001454;
 PName: P000227; Proteasome 1;
 Prostie: P000064; PROTEASOME 1;
 KW Proteasome; Hydrolyase; Peptidase;
 SEQENCE 225 AA; 24544 MW; EMBL00079F4540470 CRO64;

Query Match 0.5%; Score 57; DB 1; Length 223;
 Best Local Similarity 29.3%; Pred. No. 77;
 Matches 17, Conservative 11; Mismatches 30; Indels 0; Gaps 0;
 QY 1491 ESQEMGLGVNVEHTSKQHRKFLSVSMQLLSNNFKKVVESGPELKKHLE 1548
 DB 64 QAIWKAIGKVIKSHLIVQHQRNKMSQVMAQLLSNTLYPSPFFYYAFNVLCGLDE 121
 RESULT 187
 Y500_METJA STANDARD; PRT; 259 AA.
 AC Q57923;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0500.
 GN MJ0500.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcus.
 CC Methanococcus.
 CX NCBI_TaxID:2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: JAL-1 / DSM 2661 / ATCC 43067;
 EX MEDLINE: 96337999; PubMed: 8688087;
 RA Bult C.J., White G., Olsen G., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton P.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
 RA Overbeek R., Kirkness F.F., Weissbrock C.K., Merrick J.M., Glisbrook A.,
 RA Scott J.L., Georghiou G.S., Weidman J.F., Fuhrman J.J., Nguyen H.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hannon M.C.,
 RA Cotton M.D., Roberts K.M., Hristova M., Kalne F.P., Borodovsky M.,
 EA Klenk H.P., Fraser C.M., Smith W.R., Wren S.R., Venter J.C.
 FT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 CC Science 273:1058-1073(1996).
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 DR EMBL: U67500; AAB98491.1;
 DR TIGR: MJ0500;
 KW Hypothetical protein.
 SQ SEQUENCE 259 AA; 29192 MW; 50528A176H1C2D36 CRO64;

Query Match 0.5%; Score 57; DB 1; Length 259;
 Best Local Similarity 29.3%; Pred. No. 94;
 Matches 12, Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 QY 1835 ALKFTYKSTKZKWKWKNNQVMTSLQPHICXMKKPEELSHQS 1865
 DB 32 ALPYSVLIESNCFALCVMTLLFYPPQNPPELININEN 72
 RESULT 188
 YZ34_METJA STANDARD; PRT; 295 AA.
 AC Q60258;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ05134.
 GN MJ05134.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcus.
 CC Methanococcus.

OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL_1 / LSM 2601 / ATCC 43067,
 RX MEDLINE 96337904; PubMed 9648027;
 RA BUILD C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sulten C.G., Blake T.A., Fierapala I.M., Clayton P.A., Gocayne J.D.,
 RA Kerlavage A.P., Dougherty R.A., Tomb L.F., Adams M.F., Belcher P.L.,
 RA Overbeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glisick A.,
 RA Scott J.L., Georghan N.S.M., Weidman J.P., Fuhmann J.L., Nguyen D.,
 RA Ulterback T.P., Kelley T.M., Peterson J.P., Salfow P.W., Hannu M.P.,
 RA Clifton M.D., Roberts K.M., Hurst M.A., Kaine R.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.G., Weiss C.R., Venter J.C.,
 RI "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RI jannaschii.";
 RL Science 273:1058-1073(1996).
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 CC or send an email to license@sib-sib.ch)
 CC
 CC EMBL: L77118; AAC37103.1;
 DR TIGR: M10734;
 KW hypothetical protein.
 SQ SEQUENCE 295 AA; 4629 MW; 19197AA01092151 CRC64;

Query Match 0.54; Score 57; DB 1; Length 295;
 Best Local Similarity 22.29; Pred. No. 1,1e+02;
 Matches 12; Conservative 2; Mismatches 16; Indels 0; Gaps 0.
 QY 1625 RTGCGHNSKPKTVERFLKLVLLALVGRKKRKEGR 1650
 DB 260 RTGKSPKPTFTFTNFKLRLKLVLLVGRKKRKEGR 295

RESULT 189
 GCP_MYCGE
 ID GCP_MYCGB STANDARD; PRT; 315 AA.
 AC 647292;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROBABLE G-STALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57)
 DE (GLYCOPROTEASE).
 GN GCP OR M0046.
 GN Mycoplasma genitalium
 OS Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN AF013530 / G 27;
 RX MEDLINE 96326446; PubMed 7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Holt R.A., Kerlavage A.P., Sulten C.G., Kelley T.M.,
 RA Fierapala I.M., Weidman J.P., Small K.V., Sandosky M., Fuhmann J.L.,
 RA Ulterback T.P., Overbeck R., Scott J.L., Merrick J.M.,
 RA Tomb J.-F., Dougherty R.A., Bell P.F., Hu P.-C., Lacer T.S.,
 RA Peterson S.N., Smith H.G., Borodovsky M., Venter J.C.,
 RI "The minimal gene complement of Mycoplasma genitalium".
 RL Science 270:397-403(1995)
 CC -1- FUNCTION: COULD BE A METALLOPROTEASE
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF G-STALOGLYCOPROTEINS; CLEAVES
 CC UNRELYC-SYLATED PROTEINS. GLYCOPROTEIN A DOES NOT CLEAVE
 CC GLYCOPROTEINS THAT ARE ONLY N-GLYCOSYLATED.
 CC -1- COFACTOR: 71Nc (PROBABLY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M22; ALSO KNOWN AS THE

CC GLYCOPROTEASE FAMILY.
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 CC or send an email to license@sib-sib.ch)
 CC
 CC PMPI: U36684; AAC71262.1;
 DR TIGR: M0046;
 DR InterPro: IPR000005;
 DR Pfam: PF00814; Peptidase_M22; 1.
 DR PRINIS: PR00789; OSIALOPTASE.
 DR PROSITE: PS01016; GLYCOPROTEASE; 1.
 KW Hydrolase; Metalloprotease; zinc.
 FT METAL 110 110 ZINC (POTENTIAL).
 FT METAL 114 114 ZINC (POTENTIAL).
 SQ SEQUENCE 315 AA; 34708 MW; D186ECD176C4E574 CRC64;
 Query Match 0.54; Score 57; DB 1; Length 315;
 Best Local Similarity 28.84; Pred. No. 1,1e+02;
 Matches 15; Conservative 10; Mismatches 27; Indels 0; Gaps 0.
 QY 575 VLKIAADILKEEELSPNDGLSNQVVVCLPFVVINNDTSAEMKIAIYLS 626
 DB 256 IRETAPEMLLVGVGVANGLVSHRIETLNLEFLAISEYTSACAMIGFTAS 307

RESULT 190
 WZEB_SALTY
 ID WZEB_SALTY STANDARD; PRT; 327 AA.
 AC 004866;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CHAIN LENGTH DETERMINANT PROTEIN (POLYSACCHARIDE ANTIGEN CHAIN
 DE REGULATOR).
 GN WZEB OR OLD OR ROL.
 GN Salmonella typhimurium.
 OS Bacteria; Proteobacteria, gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN 112;
 RX MEDLINE 93225815; PubMed 7682229;
 RA Hsieh D.A., Stevenson G., Brown P., Haase A., Reeves P.R.,
 PT "Repeat unit polysaccharides of bacteria: a model for polysaccharide
 PT resembling that of ribosomes and fatty acid synthetase, with a novel
 RT mechanism for determining chain length.";
 RL Mol. Microbiol. 7:725-734(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN 112;
 RX MEDLINE 93255434; PubMed 1379582;
 RA Batchelor P.A., Allfano P., Riffali E., Hull S.L., Hull R.A.,
 FT "Polysaccharide sequences of the group O-polysaccharide
 FT antigen chain length (rol) from Escherichia coli and Salmonella
 FT typhimurium: distinct homology and functional complementation.";
 RL J. Bacteriol. 174:5228-5236(1992).
 CC -1- FUNCTION: CONFERS A MODAL DISTRIBUTION OF CHAIN LENGTH ON THE
 CC O-ANTIGEN COMPONENT OF LIPOPOLYSACCHARIDE (LPS). GIVES RISE TO
 CC A REDUCED NUMBER OF SHORT CHAIN MOLECULES AND INCREASES IN
 CC NUMBERS OF LONGER MOLECULES, WITH A MODAL VALUE OF 20.
 CC -1- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: INTROCAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE WZEB/CMD/ROL FAMILY.
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DR	EMUL; AF010032; AAC00824.1;
DR	HSSP; 600944; 21YS;
DR	EMBL; BB1276;
DR	EMBL; AF010033; AAC00824.1;

	Matches	14;	Conservative	27,	Mismatches	27,	Indels	9;	Gaps	
C7	1126	PATPPTTCTVYVQDPSGVALVSEVSTKDTLVAVASVEETITFPCAPRGGVQ	1178							

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Query Ma

Best local Similarity: 43.9%; Prod. No. 1.7e+02;
Matches: 16; Conservation: 14; Mismatches: 47; Indels: 0; Gaps: 0;

07 1795 EMASASUANRISLSAETIAETAGGVIIETAKKIVKQTEFNWNNHMDKMSUQEHGIX 1854

10 56 LFAATAEENIIVSTAEIATAAKIKLVIIPIIKRAVEHAFENIEKVHAGQMPPIHIAETEPGV 115

07 1855 MKKEELF 1861

11 111

11 116 FAGEKIT 122

RESULT 290

HS62 ASFPD

10 HS62 ASFPD

10 HS62 ASFPD

10 HS62 ASFPD

10 HS62 ASFPD

10 HS62 ASFPD

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